STIC Search Report
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TO: James Schultz
Location: REM-2D18/2C18
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Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

```
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 10466; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 17 BP; 1 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 TGCGGGTGACCGAGG 30
              ||||||||||  | ||
Db          3 TGCGGGTGACGGTGG 17
```

```
RESULT 1045
ABK94438
ID   ABK94438 standard; DNA; 17 BP.
XX
AC   ABK94438;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human MLH1 DNA mismatch repair gene, exon 18, PCR primer 18R.
XX
KW   hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;
KW   breast and ovarian cancer susceptibility gene; TGDS; human;
KW   two-dimensional DNA electrophoresis; tumour suppressor gene;
KW   breast cancer; ovarian cancer; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200236819-A1.
XX
PD   10-MAY-2002.
XX
PF   06-NOV-2000; 2000WO-IB001607.
XX
PR   06-NOV-2000; 2000WO-IB001607.
XX
PA   (SCSC-) ACAD APPLIED SCI.
XX
PI   Vijg J;
XX
DR   WPI; 2002-471507/50.
XX
PT   Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT   amplification products to 2-dimensional gel electrophoresis to produce a
PT   characteristic spot pattern for a specific mutation in either the BRCA1
PT   or the hMLH1 gene.
XX
PS   Claim 6; Page 25; 57pp; English.
XX
CC   The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC   comprising subjecting a set of amplification products to two-dimensional
CC   DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC   specific mutation in either the BRCA1 or the hMLH1 gene. Also included
CC   are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
CC   PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
CC   KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
CC   detecting mutations in the BRCA1 (breast and ovarian cancer
CC   susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA
CC   mismatch repair gene). The present sequence is a PCR primer specific to
CC   hMLH1 used in the method of the invention
XX
SQ   Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         85 CAGTGGACATCACCA 99
              |||||  ||||||||
Db          3 CAGTGTGCATCACCA 17
```

```
RESULT 1046
ABV85710
ID   ABV85710 standard; DNA; 17 BP.
XX
AC   ABV85710;
XX
DT   11-DEC-2002  (first entry)
XX
DE   Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:703.
XX
KW   Human; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10;
```

KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EP1243660-A2.
XX
PD 25-SEP-2002.
XX
PF 25-JAN-2002; 2002EP-00001161.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 30-AUG-2001; 2001US-0315984P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J, Gu Y, Nguyen C;
XX
DR WPI; 2002-724954/79.
XX
PT Nucleic acid encoding human UDP-GalNAc:polypeptide N-
PT cetylgalactosaminyltransferase 10 protein is useful to diagnose, prevent
PT and treat disorders associated with reduced or over expression of the
PT encoded protein.
XX
PS Example 2; SEQ ID NO 703; 59pp; English.
XX
CC The present invention describes an isolated nucleic acid (I) encoding a
CC human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10 (pp-
CC GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
CC present invention can be used in therapy, particularly to prevent or
CC treat a disorder associated with decreased expression or activity of pp-
CC GaNTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
CC ABP53504 are given in the exemplification of the present invention. N.B.
CC The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 17 BP; 2 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        286 CCAAGCTGGTGAAGG 300
              ||  ||||||||||| 
Db          1 CCGGGCTGGTGAAGG 15
```

RESULT 1047
ABV85709
ID ABV85709 standard; DNA; 17 BP.
XX
AC ABV85709;
XX
DT 11-DEC-2002 (first entry)
XX
DE Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:702.
XX
KW Human; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10;
KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EP1243660-A2.
XX
PD 25-SEP-2002.
XX
PF 25-JAN-2002; 2002EP-00001161.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 30-AUG-2001; 2001US-0315984P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J, Gu Y, Nguyen C;
XX
DR WPI; 2002-724954/79.
XX
PT Nucleic acid encoding human UDP-GalNAc:polypeptide N-
PT cetylgalactosaminyltransferase 10 protein is useful to diagnose, prevent
PT and treat disorders associated with reduced or over expression of the
PT encoded protein.
XX
PS Example 2; SEQ ID NO 702; 59pp; English.
XX
CC The present invention describes an isolated nucleic acid (I) encoding a
CC human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10 (pp-
CC GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
CC present invention can be used in therapy, particularly to prevent or
CC treat a disorder associated with decreased expression or activity of pp-
CC GaNTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
CC ABP53504 are given in the exemplification of the present invention. N.B.
CC The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        286 CCAAGCTGGTGAAGG 300
              ||  ||||||||||| 
Db          2 CCGGGCTGGTGAAGG 16
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RESULT 1048
ABK25243/c
ID ABK25243 standard; DNA; 17 BP.
XX
AC ABK25243;
XX
DT 09-APR-2002 (first entry)
XX
DE Male-sterile plant producing genome altering oligonucleotide #143.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyric herbicide resistance; triazine resistance; disease resistance;

KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Triticum aestivum.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017672.
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
DR WPI; 2002-106307/14.
XX
PT New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
PS Claim 7; Page 79; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyric herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 402 GTCTTCTACGTGATC 416
| ||||||| |||||
Db 16 GCCTTCTACATGATC 2

RESULT 1049
ABK25256
ID ABK25256 standard; DNA; 17 BP.
XX
AC ABK25256;
XX
DT 09-APR-2002 (first entry)
XX
DE Male-sterile plant producing genome altering oligonucleotide #156.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyric herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Zea mays.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017672.
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
DR WPI; 2002-106307/14.
XX
PT New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
PS Claim 7; Page 80; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyric herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 402 GTCTTCTACGTGATC 416
| ||||||| |||||

```
Db          2 GCCTTCTACATGATC 16


RESULT 1050
ABK25255/c
ID   ABK25255 standard; DNA; 17 BP.
XX
AC   ABK25255;
XX
DT   09-APR-2002  (first entry)
XX
DE   Male-sterile plant producing genome altering oligonucleotide #155.
XX
KW   Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW   o-methyl modification; LNA modification; phosphorothioate linkage;
KW   DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW   abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW   amino acid over production; herbicide resistance; glyphosate resistance;
KW   imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW   porphyric herbicide resistance; triazine resistance; disease resistance;
KW   modified oil production; modified starch production; waxy starch;
KW   altered floral morphology; male-sterile plant; albino mutant;
KW   modified fatty acid content; reduced palmitate production; albino plant;
KW   increased stearate production; reduced linolenic acid production;
KW   photosynthetic process.
XX
OS   Zea mays.
OS   Synthetic.
XX
PN   WO200192512-A2.
XX
PD   06-DEC-2001.
XX
PF   01-JUN-2001; 2001WO-US017672.
XX
PR   01-JUN-2000; 2000US-0208538P.
PR   30-OCT-2000; 2000US-0244989P.
PR   27-MAR-2001; 2001US-00818875.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Gamper HB,  Rice MC,  Kim J;
XX
DR   WPI; 2002-106307/14.
XX
PT   New oligonucleotides with modified nuclease-resistant termini, useful for
PT   creating plants with desired phenotypes, e.g. stress tolerance, improved
PT   nutritional value, herbicide or disease resistance, or modified oil
PT   production.
XX
PS   Claim 7; Page 80; 220pp; English.
XX
CC   The invention relates to an oligonucleotide for targeted alteration of a
CC   genetic sequence, which comprises a single-stranded oligonucleotide
CC   having a DNA domain. The DNA domain has at least one mismatch with
CC   respect to the genetic sequence to be altered and further comprises
CC   chemical modifications of the oligonucleotide. The chemical modifications
CC   consist of o-methyl modification, an LNA modification, two or more
CC   phosphorothioate linkages on a terminus, or a combination of any two or
CC   more of these modifications. The oligonucleotides are useful for
CC   directing repair or alteration of plant genetic information. The
CC   oligonucleotides are particularly useful for creating plants with desired
CC   phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC   nutritional value (e.g. altering amino acid content of plants or
CC   conferring amino acid over production), herbicide resistance (e.g.
CC   glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC   resistance, porphyric herbicide resistance or triazine resistance),
CC   disease resistance, modified oil production, modified starch production
CC   (e.g. increased starch or production of waxy starch), altered floral
CC   morphology (e.g. male-sterile plants) or modified fatty acid content
CC   (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC   The oligonucleotides are also useful for producing albino mutants for the
CC   analysis of photosynthetic processes. This sequence represents a genome
CC   altering oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        402 GTCTTCTACGTGATC 416
              | ||||||| |||||
Db         16 GCCTTCTACATGATC 2


RESULT 1051
ABK25244
ID   ABK25244 standard; DNA; 17 BP.
XX
AC   ABK25244;
XX
DT   09-APR-2002  (first entry)
XX
DE   Male-sterile plant producing genome altering oligonucleotide #144.
XX
KW   Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW   o-methyl modification; LNA modification; phosphorothioate linkage;
KW   DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW   abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW   amino acid over production; herbicide resistance; glyphosate resistance;
KW   imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW   porphyric herbicide resistance; triazine resistance; disease resistance;
KW   modified oil production; modified starch production; waxy starch;
KW   altered floral morphology; male-sterile plant; albino mutant;
KW   modified fatty acid content; reduced palmitate production; albino plant;
KW   increased stearate production; reduced linolenic acid production;
KW   photosynthetic process.
XX
OS   Triticum aestivum.
OS   Synthetic.
XX
PN   WO200192512-A2.
XX
PD   06-DEC-2001.
XX
PF   01-JUN-2001; 2001WO-US017672.
XX
PR   01-JUN-2000; 2000US-0208538P.
PR   30-OCT-2000; 2000US-0244989P.
PR   27-MAR-2001; 2001US-00818875.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Gamper HB,  Rice MC,  Kim J;
XX
DR   WPI; 2002-106307/14.
XX
PT   New oligonucleotides with modified nuclease-resistant termini, useful for
PT   creating plants with desired phenotypes, e.g. stress tolerance, improved
PT   nutritional value, herbicide or disease resistance, or modified oil
PT   production.
XX
PS   Claim 7; Page 79; 220pp; English.
XX
CC   The invention relates to an oligonucleotide for targeted alteration of a
CC   genetic sequence, which comprises a single-stranded oligonucleotide
CC   having a DNA domain. The DNA domain has at least one mismatch with
CC   respect to the genetic sequence to be altered and further comprises
CC   chemical modifications of the oligonucleotide. The chemical modifications
CC   consist of o-methyl modification, an LNA modification, two or more
CC   phosphorothioate linkages on a terminus, or a combination of any two or
CC   more of these modifications. The oligonucleotides are useful for
CC   directing repair or alteration of plant genetic information. The
CC   oligonucleotides are particularly useful for creating plants with desired
CC   phenotypes, e.g. environmental or abiotic stress tolerance, improved
```

```
CC   nutritional value (e.g. altering amino acid content of plants or
CC   conferring amino acid over production), herbicide resistance (e.g.
CC   glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC   resistance, porphyric herbicide resistance or triazine resistance),
CC   disease resistance, modified oil production, modified starch production
CC   (e.g. increased starch or production of waxy starch), altered floral
CC   morphology (e.g. male-sterile plants) or modified fatty acid content
CC   (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC   The oligonucleotides are also useful for producing albino mutants for the
CC   analysis of photosynthetic processes. This sequence represents a genome
CC   altering oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        402 GTCTTCTACGTGATC 416
              | ||||||| |||||
Db          2 GCCTTCTACATGATC 16


RESULT 1052
ABA81930
ID   ABA81930 standard; DNA; 17 BP.
XX
AC   ABA81930;
XX
DT   25-JAN-2002  (first entry)
XX
DE   Rat G-protein serotonin receptor PCR primer #26.
XX
KW   Microorganism detection; capture oligonucleotide; probe; cancer; biochip;
KW   polymorphism detection; genetic disease diagnosis; microarray;
KW   PCR primer; ss.
XX
OS   Rattus sp.
XX
PN   WO200177372-A2.
XX
PD   18-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-BE000053.
XX
PR   24-MAR-2000; 2000EP-00870055.
PR   15-SEP-2000; 2000EP-00870204.
XX
PA   (UYNO-) UNIV NOTRE-DAME DE LA PAIX.
XX
PI   Remacle J,  Hamels S,  Zammatteo N,  Lockman L,  Dufour S;
PI   Alexandre I,  De Longueville F;
XX
DR   WPI; 2002-010921/01.
XX
PT   Identifying or quantifying organisms or genes, useful e.g. for diagnosis,
PT   by detecting specific nucleotide sequences present among several
PT   homologous sequences.
XX
PS   Example 12; Page 39; 56pp; English.
XX
CC   The present invention provides a method of identifying or quantitating a
CC   microorganism in a sample by detecting its nucleotide sequence from
CC   amongst homologous sequences. The method can be used to detect
CC   microorganisms and polymorphisms, and to diagnosis genetic diseases
CC   including cancer. The present sequence is a PCR primer used in the
CC   exemplification of the invention
XX
SQ   Sequence 17 BP; 0 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        240 GGCTGCTTCCCGGGC 254
              ||||||| |||| |
Db          3 GGCTGCTTTCCGGTC 17


RESULT 1053
ABV79110
ID   ABV79110 standard; DNA; 17 BP.
XX
AC   ABV79110;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 356.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-00001167.
XX
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   23-MAY-2001; 2001US-00864761.
PR   09-OCT-2001; 2001US-0327898P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL), useful
PT   for identifying agonist and antagonist and specific binding partners, and
PT   for treating subjects having defects in HTPL.
XX
PS   Example 2; Page 110; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention
XX
SQ   Sequence 17 BP; 1 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
```

```
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        138 CGCCTGGCGGTGGAG 152
              ||||||  ||  |||||
Db          1 CGCCTGCCGCTGGAG 15


RESULT 1054
ABV78970/c
ID   ABV78970 standard; DNA; 17 BP.
XX
AC   ABV78970;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 216.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-00001167.
XX
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   23-MAY-2001; 2001US-00864761.
PR   09-OCT-2001; 2001US-0327898P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL), useful
PT   for identifying agonist and antagonist and specific binding partners, and
PT   for treating subjects having defects in HTPL.
XX
PS   Example 2; Page 92; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention
XX
SQ   Sequence 17 BP; 6 A; 7 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        236 GGGAGGCTGCTTCCC 250
              |||  |||||||| ||
Db         17 GGGTGGCTGCTTGCC 3


RESULT 1055
ABV79499
ID   ABV79499 standard; DNA; 17 BP.
XX
AC   ABV79499;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 745.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-00001167.
XX
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   23-MAY-2001; 2001US-00864761.
PR   09-OCT-2001; 2001US-0327898P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL), useful
PT   for identifying agonist and antagonist and specific binding partners, and
PT   for treating subjects having defects in HTPL.
XX
PS   Example 2; Page 161; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention
```

```
XX
SQ   Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        353 CTACAGCGACTTCCT 367
              ||||||||||  ||
Db          1 CTACAGCGACTCACT 15


RESULT 1056
ABV79553/c
ID   ABV79553 standard; DNA; 17 BP.
XX
AC   ABV79553;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 799.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-00001167.
XX
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   23-MAY-2001; 2001US-00864761.
PR   09-OCT-2001; 2001US-0327898P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL), useful
PT   for identifying agonist and antagonist and specific binding partners, and
PT   for treating subjects having defects in HTPL.
XX
PS   Example 2; Page 168; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC   skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC   clinically useful diagnostic markers and potenial therapeutic agents for
CC   male infertility and cancer. The present oligonucleotide was used in an
CC   example from the invention
XX
SQ   Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        373 TCCTGGACCGCGACG 387
              ||||| ||||||  ||
Db         15 TCCTGCACCGCGCCG 1


RESULT 1057
ABV78972/c
ID   ABV78972 standard; DNA; 17 BP.
XX
AC   ABV78972;
XX
DT   03-JAN-2003  (first entry)
XX
DE   Human HTPL scanning oligonucleotide SEQ ID 218.
XX
KW   Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW   human testis expressed Patched like protein; testis; adrenal; liver;
KW   male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW   prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1229046-A2.
XX
PD   07-AUG-2002.
XX
PF   28-JAN-2002; 2002EP-00001167.
XX
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   23-MAY-2001; 2001US-00864761.
PR   09-OCT-2001; 2001US-0327898P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhan J;
XX
DR   WPI; 2002-676582/73.
XX
PT   Novel isolated human testis expressed Patched like protein (HTPL), useful
PT   for identifying agonist and antagonist and specific binding partners, and
PT   for treating subjects having defects in HTPL.
XX
PS   Example 2; Page 92; 718pp; English.
XX
CC   The present invention relates to human testis expressed Patched like
CC   protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC   has two isoforms, with a few single base pair differences between the
CC   two. One of the single base pair changes introduces a premature stop
CC   codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC   shares an overall structure organisation with the Patched protein. The
CC   shared structural features strongly imply that HTPL plays a role similar
CC   to that of Patched, and is a potential tumour suppressor. HTPL is
CC   important in regulating male germ cell development, and the HTPL gene was
CC   mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC   useful for diagnosing a disorder caused by mutation in HTPL, and in
CC   therapy and manufacture of a medicament for treatment or prevention of
CC   such disorder associated with decreased expression or activity of human
CC   HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC   foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
```

CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 4 A; 9 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 236 GGGAGGCTGCTTCCC 250
||| ||||||||| ||
Db 15 GGGTGGCTGCTTGCC 1

RESULT 1058
ABV79497
ID ABV79497 standard; DNA; 17 BP.
XX
AC ABV79497;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 743.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 161; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 353 CTACAGCGACTTCCT 367
||||||||||| ||
Db 3 CTACAGCGACTCACT 17

RESULT 1059
ABV79106
ID ABV79106 standard; DNA; 17 BP.
XX
AC ABV79106;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 352.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 109; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in

CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 1 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 136 CCCGCCTGGCGGTGG 150
||||||| || |||
Db 3 CCCGCCTGCCGCTGG 17

RESULT 1060
ABV78971/c
ID ABV78971 standard; DNA; 17 BP.
XX
AC ABV78971;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 217.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 92; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 236 GGGAGGCTGCTTCCC 250
||| |||||||| ||
Db 16 GGGTGGCTGCTTGCC 2

RESULT 1061
ABV79498
ID ABV79498 standard; DNA; 17 BP.
XX
AC ABV79498;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 744.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 161; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 353 CTACAGCGACTTCCT 367
||||||||||| ||
Db 2 CTACAGCGACTCACT 16

RESULT 1062
ABV79552/c
ID ABV79552 standard; DNA; 17 BP.
XX
AC ABV79552;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 798.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
PT Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 168; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potenial therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 373 TCCTGGACCGCGACG 387
||||| |||||| ||
Db 16 TCCTGCACCGCGCCG 2

RESULT 1063
ABK18724
ID ABK18724 standard; RNA; 17 BP.
XX
AC ABK18724;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG DNAzyme target sequence Seq ID No 1371.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 89; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 383 CGACGACGGCGCCAA 397
||||| |||||| ||
Db 1 CGACGGCGGCGCUAA 15

RESULT 1064
ABK19125
ID ABK19125 standard; RNA; 17 BP.
XX
AC ABK19125;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG Amberzyme target sequence Seq ID No 1772.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 120; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 383 CGACGACGGCGCCAA 397
||||| |||||| ||
Db 2 CGACGGCGGCGCUAA 16

RESULT 1065
ABK17730/c
ID ABK17730 standard; RNA; 17 BP.
XX
AC ABK17730;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 377.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX

```
PI   Jarvis T,  Von Carlowitz I,  Mcswiggen JA,  Mclaughlin F,  Randi AM;
XX
DR   WPI; 2002-082995/11.
XX
PT   Novel polynucleotide which down regulates expression of Ets-related gene,
PT   useful for treating cancer, diabetic retinopathy, macular degeneration,
PT   arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS   Claim 4; Page 65; 149pp; English.
XX
CC   The invention relates to a nucleic acid molecule (I) which down regulates
CC   expression of an Ets-related gene (ERG). (I) is useful for treating
CC   conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC   tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC   neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC   vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC   Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC   syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC   treating a patient having a condition associated with the level of ERG,
CC   by contacting cells of the patient with (I) under conditions suitable for
CC   the treatment. The method comprises the use of one or more therapies
CC   under conditions suitable for the treatment. Leukaemia or tumour
CC   angiogenesis is treated by administering (I) to the patient in
CC   conjunction with one or more of other therapies such as radiation or
CC   chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC   cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC   ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC   cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC   diseases related to the expression of ERG, and as diagnostic tool to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of ERG RNA in a cell. (I) is useful for specifically
CC   targeting genes that share homology with ERG gene or ERG fusion genes.
CC   ABK17354-ABK22719 represent nucleic acids, including antisense and
CC   enzymatic nucleic acid molecules which regulate expression of ERG, and
CC   related PCR primers of the invention
XX
SQ   Sequence 17 BP; 1 A; 4 C; 6 G; 0 T; 6 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        393 GCCAAGAAGGTCTTC 407
              ||||||||||  | ||
Db         15 GCCAAGAAGGCCATC 1


RESULT 1066
ABV91236/c
ID   ABV91236 standard; DNA; 17 BP.
XX
AC   ABV91236;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 1949.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-00001165.
XX
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   23-MAY-2001; 2001US-00864761.
PR   10-OCT-2001; 2001US-0328205P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M;
XX
DR   WPI; 2002-684061/74.
XX
PT   Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT   -1, useful for treating disorders associated with decreased expression or
PT   activity of human POSHL1.
XX
PS   Example 2; SEQ ID NO 1949; 60pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated SH3 domain (POSH)-like signalling
CC   protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC   acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC   (S1) having 95% deviations, especially conservative substitutions or a
CC   fragment of the sequences comprising at least 8 contiguous amino acids.
CC   Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC   adaptor protein that interacts with Rho family small GTPases as well as
CC   downstream components of the signal transduction pathway. (I) is useful
CC   for identifying a specific binding partner. (I) and nucleic acids (II)
CC   encoding (I) are useful for diagnosing, monitoring disease and treating
CC   caused by altered expression of human POSHL1 including diagnosing and
CC   treating cancer, they useful in the development of vaccines and (II) is
CC   useful in gene therapy. (II) is useful for constructing microarrays which
CC   are useful for measuring and for surveying gene expression and creating
CC   transgenic non-human animals capable of producing the proteins. The
CC   present sequence is that of a scanning oligonucleotide useful in examples
CC   of the invention. Note: The present sequence did not form part of the
CC   printed specification, but is based on sequence information supplied to
CC   Derwent by the European Patent Office
XX
SQ   Sequence 17 BP; 2 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         92 CATCACCACGTCTGA 106
              || ||||||| ||||
Db         15 CACCACCACGGCTGA 1


RESULT 1067
ABV91234/c
ID   ABV91234 standard; DNA; 17 BP.
XX
AC   ABV91234;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human POSHL1 scanning oligonucleotide SEQ ID NO 1947.
XX
KW   Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW   Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW   gene therapy; transgenic; ss.
XX
OS   Homo sapiens.
XX
PN   EP1239051-A2.
XX
PD   11-SEP-2002.
XX
PF   28-JAN-2002; 2002EP-00001165.
XX
PR   30-JAN-2001; 2001WO-US000663.
```

PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
DR WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 1947; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 1 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

```
  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         92 CATCACCACGTCTGA 106
              || ||||||| ||||
Db         17 CACCACCACGGCTGA 3
```

RESULT 1068
ABV91235/c
ID ABV91235 standard; DNA; 17 BP.
XX
AC ABV91235;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1948.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
PN EP1239051-A2.
XX
PD 11-SEP-2002.
XX
PF 28-JAN-2002; 2002EP-00001165.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
DR WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 1948; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

```
  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         92 CATCACCACGTCTGA 106
              || ||||||| ||||
Db         16 CACCACCACGGCTGA 2
```

RESULT 1069
ABL31714
ID ABL31714 standard; DNA; 17 BP.
XX
AC ABL31714;
XX
DT 21-MAR-2002 (first entry)
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 1203.
XX
KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO200192572-A1.
XX

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PD   06-DEC-2001.
XX
PF   01-JUN-2001; 2001WO-JP004662.
XX
PR   01-JUN-2000; 2000JP-00164798.
XX
PA   (NISN ) NISSHINBO IND INC.
PA   (SYST-) SYSTEM RES INC.
XX
PI   Inoko H,  Kagiya T,  Ichihara T,  Matsumura Y,  Moriya S,  Nishida M;
XX
DR   WPI; 2002-122074/16.
XX
PT   Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT   individuals e.g. by determining immunogenetic differences when
PT   transplanting between them.
XX
PS   Claim 10; Page 321; 345pp; Japanese.
XX
CC   The invention relates to a typing kit for judging human leukocyte antigen
CC   (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC   oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC   genes e.g. belonging to HLA class I antigens on human genome and
CC   containing gene polymorphisms as alloantigens have been immobilised as
CC   primers for amplification of cleaved nucleic acids relating to gene
CC   polymorphisms. The method is useful for judging HLA genotypes of
CC   individuals by determining immunogenetic differences before transplanting
CC   between them, providing genetic information to decide compatibility of
CC   organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC   pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC   diagnosis of genetic diseases and identifying individuals
XX
SQ   Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        176 CGAGTCCAAGGCACA 190
              | || ||||||||||
Db          2 CAAGGCCAAGGCACA 16


RESULT 1070
ABK56849/c
ID   ABK56849 standard; RNA; 17 BP.
XX
AC   ABK56849;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human CLCA1 gene enzymatic nucleic acid #1220.
XX
KW   Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW   antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW   chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW   oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW   acetylcysteine.
XX
OS   Homo sapiens.
XX
PN   WO200211674-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US024970.
XX
PR   09-AUG-2000; 2000US-0224383P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (SYNT ) SYNTEX USA LLC.
PA   (THOM/) THOMPSON J.
XX
PI   Thompson J,  Mcswiggen J,  Mckenzie T,  Ayers D,  Szymkowski DE;
PI   Grupe A;
XX
DR   WPI; 2002-217145/27.
XX
PT   Enzymatic polynucleotide that down regulates expression of chloride
PT   channel calcium activated gene, useful for treating Chronic obstructive
PT   pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS   Claim 4; Page 84; 152pp; English.
XX
CC   The invention relates to enzymatic nucleic acid molecules that down
CC   regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC   by cleaving RNA derived from the genes. The nucleic acid sequences are
CC   useful as pharmaceutical agents for treating conditions such as chronic
CC   obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC   fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC   that are related to or will respond to the levels of CLCA1 in a cell or
CC   tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC   hence, are useful for treatment of a patient having a condition
CC   associated with the level of CLCA1, where the invention further comprises
CC   the use of one or more therapies under conditions suitable for the
CC   treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC   antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC   nucleic acids of the invention are also used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of CLCA1 RNA in a cell. This sequence represents an
CC   enzymatic nucleic acid molecule of the invention
XX
SQ   Sequence 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GAAACTGCGGGTGAC 25
              |||| ||||||| ||
Db         16 GAAAATGCGGGTTAC 2


RESULT 1071
ABK56242/c
ID   ABK56242 standard; RNA; 17 BP.
XX
AC   ABK56242;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human CLCA1 gene enzymatic nucleic acid #613.
XX
KW   Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW   antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW   chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW   oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW   acetylcysteine.
XX
OS   Homo sapiens.
XX
PN   WO200211674-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US024970.
XX
PR   09-AUG-2000; 2000US-0224383P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (SYNT ) SYNTEX USA LLC.
PA   (THOM/) THOMPSON J.
XX
PI   Thompson J,  Mcswiggen J,  Mckenzie T,  Ayers D,  Szymkowski DE;
PI   Grupe A;
XX
```

DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 65; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GAAACTGCGGGTGAC 25
|||| ||||||| ||
Db 17 GAAAATGCGGGTTAC 3

RESULT 1072
ABZ95233
ID ABZ95233 standard; DNA; 17 BP.
XX
AC ABZ95233;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human IL3 receptor antisense fragment no.1097.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 10475; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 17 BP; 0 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 242 CTGCTTCCCGGGCTC 256
|| ||||||||||
Db 1 CTCTTTCCCGGGCTC 15

RESULT 1073
ACC53777/c
ID ACC53777 standard; DNA; 17 BP.
XX
AC ACC53777;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human tumour suppressor sequence #2544.
XX
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
OS Homo sapiens.
XX
PN FR2826373-A1.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
DR WPI; 2003-250498/25.
XX
PT New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
PS Claim 1; Page 627; 798pp; French.
XX

CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 4 A; 6 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 200 CTCGGTGAAAGCAGA 214
|| |||||||| |||
Db 17 CTTGGTGAAAGGAGA 3

RESULT 1074
ABT37623/c
ID ABT37623 standard; DNA; 17 BP.
XX
AC ABT37623;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 3260.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 415; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 294 GTGAAGGACCTGAGC 308
|||||| |||||| |
Db 15 GTGAAGCACCTGATC 1

RESULT 1075
ABT36046/c
ID ABT36046 standard; DNA; 17 BP.
XX
AC ABT36046;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 1683.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 229; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein

```
CC   chips. The nucleic acid sequences of the invention can be used in gene
CC   therapy. This polynucleotide sequence represents a tumour suppression
CC   related human fukutin oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 7 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        367 TCACTTTCCTGGACC 381
              || |||||||||| |
Db         15 TCCCTTTCCTGGATC 1


RESULT 1076
ACA06660/c
ID   ACA06660 standard; RNA; 17 BP.
XX
AC   ACA06660;
XX
DT   03-JUN-2003  (first entry)
XX
DE   NFKB sub-unit modulating inozyme substrate #479.
XX
KW   Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW   G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW   lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW   oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW   lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW   chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW   cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW   gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW   rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW   gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW   transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW   allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
OS   Homo sapiens.
XX
PN   US2002177568-A1.
XX
PD   28-NOV-2002.
XX
PF   23-MAY-2001; 2001US-00864785.
XX
PR   07-DEC-1992;   92US-00987132.
PR   18-MAY-1994;   94US-00245466.
PR   15-AUG-1994;   94US-00291932.
PR   23-DEC-1996;   96US-00777916.
XX
PA   (STIN/) STINCHCOMB D T.
PA   (MCSW/) MCSWIGGEN J.
PA   (DRAP/) DRAPER K G.
XX
PI   Stinchcomb DT,  Mcswiggen J,  Draper KG;
XX
DR   WPI; 2003-340953/32.
XX
PT   Novel enzymatic nucleic acid molecules which down regulates expression of
PT   a sequence encoding a subunit of nuclear factor kappa B useful for
PT   treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS   Claim 3; Page 34; 72pp; English.
XX
CC   The invention describes an enzymatic nucleic acid molecule (I) which down
CC   regulates expression of a sequence encoding a subunit of nuclear factor
CC   kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC   configuration. The enzymatic nucleic acid molecule is adapted to treat
CC   cancer and is useful for down-regulating REL-A activity in a cell, for
CC   treating a patient having a condition associated with the level of REL-A.
CC   (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC   the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC   antisense nucleic acid molecules are useful for treating breast, lung,
CC   prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC   cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC   multidrug resistant cancer. The method involves use of other drug
CC   therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC   chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC   cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC   gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC   acid molecules are also useful for treating inflammatory disease such as
CC   rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC   obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC   rejection, gene therapy applications, ischaemia/reperfusion injury
CC   (central nervous system (CNS) and myocardial), glomerulonephritis,
CC   sepsis, allergic airway inflammation, inflammatory bowel disease or
CC   infection. This sequence represents the substrate of a novel enzymatic
CC   nucleic acid molecule
XX
SQ   Sequence 17 BP; 0 A; 6 C; 9 G; 0 T; 2 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        306 AGCCCCGGGGACCGC 320
              |||||||||| || |
Db         17 AGCCCCGGGGCCCCC 3


RESULT 1077
ACA06580
ID   ACA06580 standard; RNA; 17 BP.
XX
AC   ACA06580;
XX
DT   03-JUN-2003  (first entry)
XX
DE   NFKB sub-unit modulating inozyme substrate #399.
XX
KW   Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW   G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW   lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW   oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW   lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW   chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW   cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW   gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW   rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW   gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW   transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW   allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
OS   Homo sapiens.
XX
PN   US2002177568-A1.
XX
PD   28-NOV-2002.
XX
PF   23-MAY-2001; 2001US-00864785.
XX
PR   07-DEC-1992;   92US-00987132.
PR   18-MAY-1994;   94US-00245466.
PR   15-AUG-1994;   94US-00291932.
PR   23-DEC-1996;   96US-00777916.
XX
PA   (STIN/) STINCHCOMB D T.
PA   (MCSW/) MCSWIGGEN J.
PA   (DRAP/) DRAPER K G.
XX
PI   Stinchcomb DT,  Mcswiggen J,  Draper KG;
XX
DR   WPI; 2003-340953/32.
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XX
PT   Novel enzymatic nucleic acid molecules which down regulates expression of
PT   a sequence encoding a subunit of nuclear factor kappa B useful for
PT   treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS   Claim 3; Page 33; 72pp; English.
XX
CC   The invention describes an enzymatic nucleic acid molecule (I) which down
CC   regulates expression of a sequence encoding a subunit of nuclear factor
CC   kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC   configuration. The enzymatic nucleic acid molecule is adapted to treat
CC   cancer and is useful for down-regulating REL-A activity in a cell, for
CC   treating a patient having a condition associated with the level of REL-A.
CC   (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC   the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC   antisense nucleic acid molecules are useful for treating breast, lung,
CC   prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC   cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC   multidrug resistant cancer. The method involves use of other drug
CC   therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC   chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC   cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC   gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC   acid molecules are also useful for treating inflammatory disease such as
CC   rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC   obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC   rejection, gene therapy applications, ischaemia/reperfusion injury
CC   (central nervous system (CNS) and myocardial), glomerulonephritis,
CC   sepsis, allergic airway inflammation, inflammatory bowel disease or
CC   infection. This sequence represents the substrate of a novel enzymatic
CC   nucleic acid molecule
XX
SQ   Sequence 17 BP; 4 A; 4 C; 8 G; 0 T; 1 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 5e+02;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        286 CCAAGCTGGTGAAGG 300
              ||| ||:|| |||||
Db          3 CCAGGCUGGGGAAGG 17


RESULT 1078
ACA06587/c
ID   ACA06587 standard; RNA; 17 BP.
XX
AC   ACA06587;
XX
DT   03-JUN-2003  (first entry)
XX
DE   NFKB sub-unit modulating inozyme substrate #406.
XX
KW   Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW   G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW   lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW   oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW   lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW   chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW   cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW   gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW   rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW   gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW   transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW   allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
OS   Homo sapiens.
XX
PN   US2002177568-A1.
XX
PD   28-NOV-2002.
XX
PF   23-MAY-2001; 2001US-00864785.
XX
PR   07-DEC-1992;   92US-00987132.
PR   18-MAY-1994;   94US-00245466.
PR   15-AUG-1994;   94US-00291932.
PR   23-DEC-1996;   96US-00777916.
XX
PA   (STIN/) STINCHCOMB D T.
PA   (MCSW/) MCSWIGGEN J.
PA   (DRAP/) DRAPER K G.
XX
PI   Stinchcomb DT,  Mcswiggen J,  Draper KG;
XX
DR   WPI; 2003-340953/32.
XX
PT   Novel enzymatic nucleic acid molecules which down regulates expression of
PT   a sequence encoding a subunit of nuclear factor kappa B useful for
PT   treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS   Claim 3; Page 33; 72pp; English.
XX
CC   The invention describes an enzymatic nucleic acid molecule (I) which down
CC   regulates expression of a sequence encoding a subunit of nuclear factor
CC   kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC   configuration. The enzymatic nucleic acid molecule is adapted to treat
CC   cancer and is useful for down-regulating REL-A activity in a cell, for
CC   treating a patient having a condition associated with the level of REL-A.
CC   (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC   the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC   antisense nucleic acid molecules are useful for treating breast, lung,
CC   prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC   cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC   multidrug resistant cancer. The method involves use of other drug
CC   therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC   chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC   cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC   gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC   acid molecules are also useful for treating inflammatory disease such as
CC   rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC   obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC   rejection, gene therapy applications, ischaemia/reperfusion injury
CC   (central nervous system (CNS) and myocardial), glomerulonephritis,
CC   sepsis, allergic airway inflammation, inflammatory bowel disease or
CC   infection. This sequence represents the substrate of a novel enzymatic
CC   nucleic acid molecule
XX
SQ   Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        265 TGCACCTGGAGCAGG 279
              |||| ||| ||||||
Db         15 TGCAGCTGCAGCAGG 1


RESULT 1079
ADB02422
ID   ADB02422 standard; DNA; 17 BP.
XX
AC   ADB02422;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ4 scanning oligonucleotide SEQ ID 3408.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 3408; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        363 TTCCTCACTTTCCTG 377
              ||||| ||| |||||
Db          2 TTCCTGACTATCCTG 16


RESULT 1080
ADA99249/c
ID   ADA99249 standard; DNA; 17 BP.
XX
AC   ADA99249;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 238.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 238; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 5 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         61 AGTCTCTGCACTACG 75
              ||||||| |||| |
Db         17 AGTCTCTGGACTAGG 3


RESULT 1081
ADA99251/c
ID   ADA99251 standard; DNA; 17 BP.
XX
AC   ADA99251;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 240.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
```

```
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 240; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         61 AGTCTCTGCACTACG 75
              ||||||| |||| |
Db         15 AGTCTCTGGACTAGG 1


RESULT 1082
ADB03562/c
ID   ADB03562 standard; DNA; 17 BP.
XX
AC   ADB03562;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 4548.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 4548; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        330 GCGGACGACCAGGGC 344
              ||||| | |||||||
Db         16 GCGGATGTCCAGGGC 2


RESULT 1083
ADA99250/c
ID   ADA99250 standard; DNA; 17 BP.
XX
AC   ADA99250;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 239.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 239; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
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CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         61 AGTCTCTGCACTACG 75
              ||||||| |||| |
Db         16 AGTCTCTGGACTAGG 2


RESULT 1084
ADB02423
ID   ADB02423 standard; DNA; 17 BP.
XX
AC   ADB02423;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ4 scanning oligonucleotide SEQ ID 3409.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 3409; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        363 TTCCTCACTTTCCTG 377
              ||||| ||| |||||
Db          1 TTCCTGACTATCCTG 15


RESULT 1085
ADB03563/c
ID   ADB03563 standard; DNA; 17 BP.
XX
AC   ADB03563;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 4549.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 4549; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        330 GCGGACGACCAGGGC 344
              ||||| | |||||||
Db         15 GCGGATGTCCAGGGC 1
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```
RESULT 1086
ADA99409
ID   ADA99409 standard; DNA; 17 BP.
XX
AC   ADA99409;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 398.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 398; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        361 ACTTCCTCACTTTCC 375
              | |||||||||| |||
Db          3 AGTTCCTCACTATCC 17


RESULT 1087
ADB03561/c
ID   ADB03561 standard; DNA; 17 BP.
XX
AC   ADB03561;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 4547.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 4547; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        330 GCGGACGACCAGGGC 344
              ||||| | |||||||
Db         17 GCGGATGTCCAGGGC 3


RESULT 1088
ABZ61741/c
ID   ABZ61741 standard; RNA; 17 BP.
XX
AC   ABZ61741;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human H-Ras DNAzyme target #532.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 58; Page 121; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 2 A; 7 C; 5 G; 0 T; 3 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        237 GGAGGCTGCTTCCCG 251
              ||||||||||  |||
Db         17 GGAGGCTGCTGACCG 3


RESULT 1089
ABZ65141
ID   ABZ65141 standard; RNA; 17 BP.
XX
AC   ABZ65141;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human HER2 DNAzyme substrate #598.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 4; Page 144; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   73.3%;  Pred. No. 5e+02;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        261 ACGGTGCACCTGGAG 275
              ||||:||| |:|| |
Db          1 ACGGUGCAGCUGGUG 15


RESULT 1090
ABZ64812
ID   ABZ64812 standard; RNA; 17 BP.
XX
AC   ABZ64812;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human HER2 DNAzyme substrate #269.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 4; Page 138; 185pp; English.
```

```
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 6 A; 2 C; 7 G; 0 T; 2 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 5e+02;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        203 GGTGAAAGCAGAGAA 217
              ||:|| ||||||| |
Db          2 GGUGACAGCAGAGGA 16


RESULT 1091
ABZ61416
ID   ABZ61416 standard; RNA; 17 BP.
XX
AC   ABZ61416;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human H-Ras DNAzyme target #207.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 58; Page 115; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 2 A; 8 C; 7 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        250 CGGGCTCGGCCACGG 264
              ||| | |||||||||
Db          1 CGGCCGCGGCCACGG 15


RESULT 1092
ABZ61329
ID   ABZ61329 standard; RNA; 17 BP.
XX
AC   ABZ61329;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human H-Ras DNAzyme target #120.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 58; Page 113; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 0 A; 10 C; 6 G; 0 T; 1 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 5e+02;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        250 CGGGCTCGGCCACGG 264
              ||| |:||||| |||
```

```
Db          1 CGGCCUCGGCCCCGG 15


RESULT 1093
ABZ61742/c
ID   ABZ61742 standard; RNA; 17 BP.
XX
AC   ABZ61742;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human H-Ras DNAzyme target #533.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 58; Page 121; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        236 GGGAGGCTGCTTCCC 250
              ||||||||||  ||
Db         15 GGGAGGCTGCTGACC 1


RESULT 1094
ACD60765/c
ID   ACD60765 standard; RNA; 17 BP.
XX
AC   ACD60765;
XX
DT   24-SEP-2003  (first entry)
XX
DE   HCV DNAzyme substrate sequence #2007.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 269; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GAAACTGCGGGTGAC 25
              ||||| |||||||  |
```

```
Db         16 GAAACAGCGGGTGTC 2


RESULT 1095
ACD57732
ID   ACD57732 standard; RNA; 17 BP.
XX
AC   ACD57732;
XX
DT   23-SEP-2003  (first entry)
XX
DE   HCV DNAzyme substrate sequence #486.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 242; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 3 A; 7 C; 7 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        108 CGCGACCGCAGCAAG 122
              |||| |||| |||||
Db          2 CGCGGCCGCCGCAAG 16


RESULT 1096
ACD63967
ID   ACD63967 standard; RNA; 17 BP.
XX
AC   ACD63967;
XX
DT   30-SEP-2003  (first entry)
XX
DE   HCV minus strand DNAzyme substrate sequence #1326.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 298; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
```

```
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 6 A; 6 C; 4 G; 0 T; 1 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 5e+02;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         39 GAAGATGGCCACCAC 53
              |||||:| |||| ||
Db          3 GAAGAUGCCCACAAC 17


RESULT 1097
ACD58702/c
ID   ACD58702 standard; RNA; 17 BP.
XX
AC   ACD58702;
XX
DT   24-SEP-2003  (first entry)
XX
DE   HCV DNAzyme substrate sequence #952.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 251; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 5 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         39 GAAGATGGCCACCAC 53
              ||||||| |||| ||
Db         16 GAAGATGCCCACAAC 2


RESULT 1098
ACD61848
ID   ACD61848 standard; RNA; 17 BP.
XX
AC   ACD61848;
XX
DT   23-SEP-2003  (first entry)
XX
DE   HCV minus strand DNAzyme substrate sequence #271.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
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PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 279; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 4 A; 4 C; 6 G; 0 T; 3 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 5e+02;
  Matches   12;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GAAACTGCGGGTGAC 25
              ||||| |||||:| |
Db          3 GAAACAGCGGGUGUC 17


RESULT 1099
ACD64937/c
ID   ACD64937 standard; RNA; 17 BP.
XX
AC   ACD64937;
XX
DT   30-SEP-2003  (first entry)
XX
DE   HCV minus strand DNAzyme substrate sequence #1792.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 307; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 7 C; 8 G; 0 T; 2 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        108 CGCGACCGCAGCAAG 122
              |||| |||| |||||
Db         17 CGCGGCCGCCGCAAG 3


RESULT 1100
ACC65050
ID   ACC65050 standard; DNA; 17 BP.
XX
AC   ACC65050;
XX
DT   01-JUL-2003  (first entry)
XX
DE   Murine oligonucleotide associated with tumour supression, SEQ ID 2297.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW   tumour suppression; tumour reversion; apoptosis; virus resistance;
KW   viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW   schizophrenia; ss.
XX
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OS   Mus musculus.
XX
PN   WO2003025176-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004210.
XX
PR   17-SEP-2001; 2001FR-00011979.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-333167/31.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; Page 299; 738pp; French.
XX
CC   The present invention relates to murine oligonucleotides (ACC62754-
CC   ACC68806), which are associated with tumour suppression, tumour
CC   reversion, apoptosis and virus resistance. The oligonucleotides are
CC   useful as (1) as probes and primers for detecting, identifying,
CC   quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC   gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC   recombinant polypeptides. The oligonucleotides are useful for preparation
CC   of pharmaceuticals for prevention and/or treatment of viral diseases that
CC   are characterised by development of tumours or cell degeneration,
CC   specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ   Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        192 ATCCACTGCTCGGTG 206
              |||| | ||||||||
Db          2 ATCCTCAGCTCGGTG 16


RESULT 1101
ACC84062
ID   ACC84062 standard; DNA; 17 BP.
XX
AC   ACC84062;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Human cytochrome P450 gene CYP2D6 reverse PCR primer A6.
XX
KW   Differential amplification of polymorphisms; DAP; human; CYP2D6;
KW   cytochrome P450; polymorphism; haplotype; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003046206-A2.
XX
PD   05-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038278.
XX
PR   28-NOV-2001; 2001US-0334046P.
XX
PA   (MJBI-) MJ BIOWORKS INC.
XX
PI   Wang Y,  Xi L,  Finney M,  Chen F;
XX
DR   WPI; 2003-482525/45.
XX
PT   Determining allelic DNA sequences and haplotypes in a DNA sample,
PT   comprises using primers with a single difference corresponding to a
PT   polymorphic site combined with quantitative PCR using a fluorescent
PT   readout.
XX
PS   Example 1; Page 22; 36pp; English.
XX
CC   The present sequence is that of primer A6, which is one of a set of
CC   primers (see ACC84057-62) used in an example of the method of the
CC   invention, i.e. differential amplification of polymorphisms (DAP), to
CC   distinguish 4 templates that differed at a single position. A 475 bp
CC   portion of the human P450 gene CYP2D6 was amplified using primer A1
CC   (forward) and A5 (reverse) and cloned into a TA cloning vector. 3 PCR
CC   primers (A2-A4) identical to A1 except for a single difference at their
CC   3' terminal bases were used with A5 to re-amplify the CYP2D6 fragment,
CC   generating the point mutations A, C and T at nucleotide 3280 (G is
CC   present in the most common allele). The 3 amplicons were cloned into TA
CC   cloning vector. In order to examine the effect of amplicon size, an
CC   additional reverse primer, A6, was used to generate a 57 bp amplicon. DAP
CC   was performed and was able to distinguish between the 4 templates. The
CC   method combines allele-specific PCR with technology used for quantitative
CC   PCR. It can be used to score the presence or absence of particular
CC   polymorphisms or particular haplotypes in a DNA sample
XX
SQ   Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        353 CTACAGCGACTTCCT 367
              || |||||||||| |
Db          1 CTCCAGCGACTTCTT 15


RESULT 1102
ACC83872
ID   ACC83872 standard; DNA; 17 BP.
XX
AC   ACC83872;
XX
DT   08-SEP-2003  (first entry)
XX
DE   Human cytochrome P450 gene CYP2D6 reverse PCR primer R1.
XX
KW   Human; cytochrome P450; CYP2D6; nucleic acid detection; error correction;
KW   single nucleotide polymorphism; SNP; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003046208-A2.
XX
PD   05-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038435.
XX
PR   28-NOV-2001; 2001US-0334032P.
XX
PA   (MJBI-) MJ BIOWORKS INC.
XX
PI   Wang Y,  Finney M,  Chen F;
XX
DR   WPI; 2003-505210/47.
XX
PT   Identifying polymorphisms using an error correcting assay that utilizes
PT   an improved generation of nucleic acid polymerases and multiplexing the
PT   assay.
XX
PS   Example 1; Page 21; 35pp; English.
XX
CC   The present primer is a reverse primer for the PCR amplification of the
CC   human cytochrome P450 CYP2D6 gene. It was used in an example from the
CC   invention in which modified error-correcting polymerases were shown to be
```

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CC   superior to unmodified error-correcting polymerases in amplifying genomic
CC   DNA from low copy number templates. The enzymes tested were Pfu DNA
CC   polymerase and PfS, a fusion of Sso7d to the C-terminus of Pfu. PfS was
CC   found to require 1/4 to 1/10 as many units as Pfu for efficient
CC   amplification. The invention provides a method of detecting
CC   polymorphisms, e.g. single nucleotide polymorphisms, by amplification and
CC   error correction using polymerases improved by the addition of a sequence
CC   -non-specific nucleic acid-binding domain that enhances the ability of
CC   the enzyme to bind and catalytically modify the nucleic acid
XX
SQ   Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        353 CTACAGCGACTTCCT 367
              || |||||||||| |
Db          1 CTCCAGCGACTTCTT 15


RESULT 1103
ADB40520
ID   ADB40520 standard; DNA; 17 BP.
XX
AC   ADB40520;
XX
DT   18-DEC-2003  (revised)
DT   04-DEC-2003  (first entry)
XX
DE   Tumour suppression/reversion associated nucleotide #843.
XX
KW   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW   primer; probe; tumour suppression; tumour reversion; apoptosis;
KW   virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2003040369-A2.
XX
PD   15-MAY-2003.
XX
PF   17-SEP-2002; 2002WO-IB004219.
XX
PR   17-SEP-2001; 2001FR-00011981.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-441574/41.
XX
PT   New nucleic acid encoding human prostate membrane-specific antigen,
PT   useful e.g. for treatment of tumors and viral infection, also related
PT   polypeptide and antibodies.
XX
PS   Disclosure; Page 130; 771pp; French.
XX
CC   The invention relates to the isolation of 6327 nucleotide sequences,
CC   fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC   sequence having at least 80% identity, after optimal alignment, with the
CC   nucleotides, a sequence that hybridizes under stringent conditions with
CC   the nucleotides, or the complement, or corresponding RNA, of the
CC   nucleotides. The nucleotides are used as probes or primers for detecting,
CC   identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC   sense and antisense sequences, of nucleotides involved in tumour
CC   suppression or reversion, apoptosis and or viral resistance, to produce
CC   recombinant polypeptides, and to prepare transgenic animals, as
CC   experimental models. The nucleotides (also vectors containing them and
CC   cells containing the vectors), the encoded polypeptides and antibodies
CC   (Ab) against the polypeptide are useful for prevention and/or treatment
CC   of viral infections or diseases characterized by development of tumours
CC   or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC   Analysis of the expression of the nucleotides can be used for diagnosis
CC   and/or prognosis of these diseases. The nucleotides and polypeptides can
CC   also be used to screen for their specific interactive molecules,
CC   potentially useful for treating diseases associated with abnormal
CC   expression of the nucleotides.
XX
SQ   Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        300 GACCTGAGCCCCGGG 314
              || |||||||| |||
Db          1 GATCTGAGCCCTGGG 15


RESULT 1104
ADC04254/c
ID   ADC04254 standard; DNA; 17 BP.
XX
AC   ADC04254;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human Na/H exchanger-like protein 1 gene oligonucleotide #701.
XX
KW   ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW   NHELP1; passive replacement therapy; vaccine; diagnosis.
XX
OS   Homo sapiens.
XX
PN   EP1273660-A2.
XX
PD   08-JAN-2003.
XX
PF   25-JAN-2002; 2002EP-00001160.
XX
PR   30-JAN-2001; 2001WO-US000666.
PR   23-MAY-2001; 2001US-00864761.
PR   21-DEC-2001; 2001US-0343331P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y;
XX
DR   WPI; 2003-302724/30.
XX
PT   New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as a
PT   passive replacement therapy or as a vaccine for treating or preventing
PT   disorders associated with aberrant expression or activity of human
PT   NHELP1.
XX
PS   Example 2; SEQ ID NO 741; 468pp; English.
XX
CC   The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC   exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
CC   polypeptide, an antibody against the protein or its antigen-binding
CC   fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
CC   polypeptide and an agonist are particularly useful for manufacturing a
CC   medicament for treating or preventing a disorder associated with
CC   decreased expression or activity of human NHELP1. The antibody or its
CC   antigen-binding fragment, and an antagonist, are useful for manufacturing
CC   a medicament for treating or preventing a disorder associated with
CC   increased expression or activity of human NHELP1. The NHELP1 nucleic acid
CC   or protein is useful as passive replacement therapy, as a vaccine, or in
CC   diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
CC   spanning the sequence of the human NHELP1 gene (ADC03514).
XX
SQ   Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
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  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         40 AAGATGGCCACCACT 54
              || ||||||| ||||
Db         17 AAAATGGCCAGCACT 3


RESULT 1105
ADC04257/c
ID   ADC04257 standard; DNA; 17 BP.
XX
AC   ADC04257;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human Na/H exchanger-like protein 1 gene oligonucleotide #704.
XX
KW   ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW   NHELP1; passive replacement therapy; vaccine; diagnosis.
XX
OS   Homo sapiens.
XX
PN   EP1273660-A2.
XX
PD   08-JAN-2003.
XX
PF   25-JAN-2002; 2002EP-00001160.
XX
PR   30-JAN-2001; 2001WO-US000666.
PR   23-MAY-2001; 2001US-00864761.
PR   21-DEC-2001; 2001US-0343331P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y;
XX
DR   WPI; 2003-302724/30.
XX
PT   New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as a
PT   passive replacement therapy or as a vaccine for treating or preventing
PT   disorders associated with aberrant expression or activity of human
PT   NHELP1.
XX
PS   Example 2; SEQ ID NO 744; 468pp; English.
XX
CC   The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC   exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
CC   polypeptide, an antibody against the protein or its antigen-binding
CC   fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
CC   polypeptide and an agonist are particularly useful for manufacturing a
CC   medicament for treating or preventing a disorder associated with
CC   decreased expression or activity of human NHELP1. The antibody or its
CC   antigen-binding fragment, and an antagonist, are useful for manufacturing
CC   a medicament for treating or preventing a disorder associated with
CC   increased expression or activity of human NHELP1. The NHELP1 nucleic acid
CC   or protein is useful as passive replacement therapy, as a vaccine, or in
CC   diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
CC   spanning the sequence of the human NHELP1 gene (ADC03514).
XX
SQ   Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         39 GAAGATGGCCACCAC 53
              ||| ||||||| |||
Db         15 GAAAATGGCCAGCAC 1


RESULT 1106
ADC98354
ID   ADC98354 standard; DNA; 17 BP.
XX
AC   ADC98354;
XX
DT   01-JAN-2004  (first entry)
XX
DE   ACLP10 polymorphism marker PCR primer B primer seq.
XX
KW   low bone mineral density; BMD; bone damage; polymorphism; osteoporosis;
KW   single nucleotide polymorphism; SNP; PCR primer; ss; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003054218-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US040948.
XX
PR   20-DEC-2001; 2001US-0342711P.
PR   04-NOV-2002; 2002US-0423559P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jones KA,  Valdes A,  Townley DJ,  Mangion J,  Galwey N,  Bennett S;
PI   Mckay I,  Schafer A;
XX
DR   WPI; 2003-559156/52.
XX
PT   Determining whether an individual is predisposed to susceptibility to low
PT   bone mineral density (BMD) and/or bone damage, involves identifying
PT   polymorphisms in associated genes.
XX
PS   Example 8; Page 237; 246pp; English.
XX
CC   The present invention describes a method of determining whether an
CC   individual is predisposed to susceptibility to low bone mineral density
CC   (BMD) and/or bone damage comprising identifying whether the individual
CC   has at least one polymorphism in a polynucleotide encoding a protein,
CC   where the polynucleotide is one of 81 200-500 nucleotide sequences (S1,
CC   see ADC98235 to ADC98315). An agent identified in an method from the
CC   present invention which can be used for the prevention or treatment of a
CC   disease resulting in susceptibility to low BMD and/or bone damage is
CC   useful in the manufacture of a medicament for use in modulating the
CC   susceptibility to low BMD and/or bone damage. The disease associated with
CC   low BMD and/or bone damage is osteoporosis. The present PCR primer
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         54 TCAGAGGAGTCTCTG 68
              ||| ||||| |||||
Db          3 TCACAGGAGGCTCTG 17


RESULT 1107
ADD19944
ID   ADD19944 standard; DNA; 17 BP.
XX
AC   ADD19944;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Oreochromis niloticus microsatellite primer  SEQ ID NO:579.
XX
KW   single nucleotide polymorphism; SNP; fish; Salmo salar;
KW   Orechromis niloticus; Atlantic halibut; microsatellite; cod;
KW   polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
```

```
KW   detection; primer; ss.
XX
OS   Synthetic.
OS   Oreochromis niloticus.
XX
PN   WO2003060160-A2.
XX
PD   24-JUL-2003.
XX
PF   17-JAN-2003; 2003WO-IB000112.
XX
PR   18-JAN-2002; 2002US-0349950P.
PR   16-AUG-2002; 2002US-0404200P.
XX
PA   (GENO-) GENOMAR ASA.
XX
PI   Lie O,  Slettan A,  Hoyum M,  Lingaas F;
XX
DR   WPI; 2003-627388/59.
XX
PT   Novel isolated nucleic acid molecule comprising single nucleotide
PT   polymorphism associated with fish, useful for forming PCR primers which
PT   are used for detecting single nucleotide polymorphisms in fish nucleic
PT   acids.
XX
PS   Claim 18; SEQ ID NO 579; 233pp; English.
XX
CC   The present invention describes an isolated nucleic acid (I) comprising a
CC   single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC   Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC   and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC   (i), or its complement under highly stringent hybridisation conditions.
CC   Also described: (1) an isolated oligonucleotide (II) comprising at least
CC   17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites, or their complement; (2)
CC   a primer pair (III) suitable for use in PCR, comprising two (II) capable
CC   of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites; and determining (M1) the
CC   origin of fish sample comprising providing a parentage genotype database
CC   comprising a collection of candidate parent genotypes, where each of the
CC   candidate parent genotype represents a distinct origin, and comparing a
CC   sample genotype to the parentage genotype database, where a match between
CC   the sample genotype and one of the candidate parent genotype identifies
CC   to the origin of the sample. (M1) is useful for determining the origin of
CC   a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC   rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC   detecting nucleic acid molecule comprising SNP in a sample, which
CC   involves contacting the sample containing nucleic acids with one or more
CC   (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
CC   SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC   useful for detecting nucleic acid molecule comprising a polymorphic
CC   sequence in a sample, comprising contacting the sample containing nucleic
CC   acids with one or more (II) which is derived from O. niloticus
CC   microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
CC   sites or seabass polymorphic sites, and identifying a nucleic acid that
CC   hybridises to (II). (III) is useful for detecting nucleic acid molecule
CC   comprising a microsatellite sequence in sample. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 17 BP; 6 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         82 GCGCAGTGGACATCA 96
              | |||| ||||||||
Db          2 GGGCAGAGGACATCA 16


RESULT 1108
ADD20889
ID   ADD20889 standard; DNA; 17 BP.
XX
AC   ADD20889;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human GAP_N DNA 17-mer oligo #121.
XX
KW   gene therapy; antibody therapy; modulator of GAPN;
KW   GTP-activator for Rab-like GTPase; GAP_N; immunogen; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003033703-A2.
XX
PD   24-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032597.
XX
PR   15-OCT-2001; 2001US-0330323P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-403224/38.
XX
PT   Novel human GTP-activator protein for Rab-like GTPase and polynucleotide
PT   encoding the protein, useful for diagnosing, treating or preventing
PT   disorders associated with increased expression or activity of the
PT   protein.
XX
PS   Example 2; SEQ ID NO 145; 149pp; English.
XX
CC   The invention relates to an isolated human GTP-activator protein for Rab-
CC   like GTPase (GAPN) polypeptide (I), a sequence having 65% identity to
CC   (I), a sequence in which at least 95% of deviations from (I) are
CC   conservative substitutions, or a fragment of at least 8 contiguous amino
CC   acids of (I). The polypeptide is useful for identifying a specific
CC   binding partner for itself, by contacting the polypeptide in vivo to a
CC   potential binding partner and determining if the polypeptide binding
CC   partner binds to the polypeptide. (I) and a nucleic acid encoding the
CC   polypeptide (II) are useful for diagnosing or monitoring a disease caused
CC   by altered expression of GAPN, by determining the level of expression of
CC   GAPN in a sample of nucleic acids or proteins that derives from a subject
CC   suspected to have the disease, alterations from a normal level of
CC   expression providing diagnostic and/or monitoring information. (I), (II)
CC   or agonist of (I) is useful for treating or preventing a disorder
CC   associated with decreased expression or activity of GAPN, and an
CC   antagonist of (I) is useful for treating or preventing a disorder
CC   associated with increased expression or activity of GAPN (all claimed).
CC   (I) is useful as immunogen to raise antibodies that specifically
CC   recognize GAPN proteins. (II) is useful to drive in vivo expression of
CC   GAPN proteins, and as hybridization probes to detect, characterize and
CC   quantify GAPN nucleic acids in and isolate GAPN nucleic acids from both
CC   genomic and transcript-derived nucleic acid samples. This sequence
CC   represents a 17-mer oligonucleotide spanning the GAP_N DNA sequence.
XX
SQ   Sequence 17 BP; 3 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        383 CGACGACGGCGCCAA 397
              ||||||| |||| |
Db          1 CGACGACGCCGCCTA 15


RESULT 1109
ADD21032/c
ID   ADD21032 standard; DNA; 17 BP.
```

XX
AC ADD21032;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human GAP_N DNA 17-mer oligo #264.
XX
KW gene therapy; antibody therapy; modulator of GAPN;
KW GTP-activator for Rab-like GTPase; GAP_N; immunogen; ss.
XX
OS Homo sapiens.
XX
PN WO2003033703-A2.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032597.
XX
PR 15-OCT-2001; 2001US-0330323P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-403224/38.
XX
PT Novel human GTP-activator protein for Rab-like GTPase and polynucleotide
PT encoding the protein, useful for diagnosing, treating or preventing
PT disorders associated with increased expression or activity of the
PT protein.
XX
PS Example 2; SEQ ID NO 288; 149pp; English.
XX
CC The invention relates to an isolated human GTP-activator protein for Rab-
CC like GTPase (GAPN) polypeptide (I), a sequence having 65% identity to
CC (I), a sequence in which at least 95% of deviations from (I) are
CC conservative substitutions, or a fragment of at least 8 contiguous amino
CC acids of (I). The polypeptide is useful for identifying a specific
CC binding partner for itself, by contacting the polypeptide in vivo to a
CC potential binding partner and determining if the polypeptide binding
CC partner binds to the polypeptide. (I) and a nucleic acid encoding the
CC polypeptide (II) are useful for diagnosing or monitoring a disease caused
CC by altered expression of GAPN, by determining the level of expression of
CC GAPN in a sample of nucleic acids or proteins that derives from a subject
CC suspected to have the disease, alterations from a normal level of
CC expression providing diagnostic and/or monitoring information. (I), (II)
CC or agonist of (I) is useful for treating or preventing a disorder
CC associated with decreased expression or activity of GAPN, and an
CC antagonist of (I) is useful for treating or preventing a disorder
CC associated with increased expression or activity of GAPN (all claimed).
CC (I) is useful as immunogen to raise antibodies that specifically
CC recognize GAPN proteins. (II) is useful to drive in vivo expression of
CC GAPN proteins, and as hybridization probes to detect, characterize and
CC quantify GAPN nucleic acids in and isolate GAPN nucleic acids from both
CC genomic and transcript-derived nucleic acid samples. This sequence
CC represents a 17-mer oligonucleotide spanning the GAP_N DNA sequence.
XX
SQ Sequence 17 BP; 2 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 256 CGGCCACGGTGCACC 270
||| |||||||| ||
Db 16 CGGGCACGGTGCTCC 2

RESULT 1110
ADD20887
ID ADD20887 standard; DNA; 17 BP.
XX
AC ADD20887;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human GAP_N DNA 17-mer oligo #119.
XX
KW gene therapy; antibody therapy; modulator of GAPN;
KW GTP-activator for Rab-like GTPase; GAP_N; immunogen; ss.
XX
OS Homo sapiens.
XX
PN WO2003033703-A2.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032597.
XX
PR 15-OCT-2001; 2001US-0330323P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-403224/38.
XX
PT Novel human GTP-activator protein for Rab-like GTPase and polynucleotide
PT encoding the protein, useful for diagnosing, treating or preventing
PT disorders associated with increased expression or activity of the
PT protein.
XX
PS Example 2; SEQ ID NO 143; 149pp; English.
XX
CC The invention relates to an isolated human GTP-activator protein for Rab-
CC like GTPase (GAPN) polypeptide (I), a sequence having 65% identity to
CC (I), a sequence in which at least 95% of deviations from (I) are
CC conservative substitutions, or a fragment of at least 8 contiguous amino
CC acids of (I). The polypeptide is useful for identifying a specific
CC binding partner for itself, by contacting the polypeptide in vivo to a
CC potential binding partner and determining if the polypeptide binding
CC partner binds to the polypeptide. (I) and a nucleic acid encoding the
CC polypeptide (II) are useful for diagnosing or monitoring a disease caused
CC by altered expression of GAPN, by determining the level of expression of
CC GAPN in a sample of nucleic acids or proteins that derives from a subject
CC suspected to have the disease, alterations from a normal level of
CC expression providing diagnostic and/or monitoring information. (I), (II)
CC or agonist of (I) is useful for treating or preventing a disorder
CC associated with decreased expression or activity of GAPN, and an
CC antagonist of (I) is useful for treating or preventing a disorder
CC associated with increased expression or activity of GAPN (all claimed).
CC (I) is useful as immunogen to raise antibodies that specifically
CC recognize GAPN proteins. (II) is useful to drive in vivo expression of
CC GAPN proteins, and as hybridization probes to detect, characterize and
CC quantify GAPN nucleic acids in and isolate GAPN nucleic acids from both
CC genomic and transcript-derived nucleic acid samples. This sequence
CC represents a 17-mer oligonucleotide spanning the GAP_N DNA sequence.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 383 CGACGACGGCGCCAA 397
||||||| |||| |
Db 3 CGACGACGCCGCCTA 17

RESULT 1111
ADD20930/c
ID ADD20930 standard; DNA; 17 BP.
XX
AC ADD20930;
XX
DT 15-JAN-2004 (first entry)

```
XX
DE   Human GAP_N DNA 17-mer oligo #162.
XX
KW   gene therapy; antibody therapy; modulator of GAPN;
KW   GTP-activator for Rab-like GTPase; GAP_N; immunogen; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003033703-A2.
XX
PD   24-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032597.
XX
PR   15-OCT-2001; 2001US-0330323P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-403224/38.
XX
PT   Novel human GTP-activator protein for Rab-like GTPase and polynucleotide
PT   encoding the protein, useful for diagnosing, treating or preventing
PT   disorders associated with increased expression or activity of the
PT   protein.
XX
PS   Example 2; SEQ ID NO 186; 149pp; English.
XX
CC   The invention relates to an isolated human GTP-activator protein for Rab-
CC   like GTPase (GAPN) polypeptide (I), a sequence having 65% identity to
CC   (I), a sequence in which at least 95% of deviations from (I) are
CC   conservative substitutions, or a fragment of at least 8 contiguous amino
CC   acids of (I). The polypeptide is useful for identifying a specific
CC   binding partner for itself, by contacting the polypeptide in vivo to a
CC   potential binding partner and determining if the polypeptide binding
CC   partner binds to the polypeptide. (I) and a nucleic acid encoding the
CC   polypeptide (II) are useful for diagnosing or monitoring a disease caused
CC   by altered expression of GAPN, by determining the level of expression of
CC   GAPN in a sample of nucleic acids or proteins that derives from a subject
CC   suspected to have the disease, alterations from a normal level of
CC   expression providing diagnostic and/or monitoring information. (I), (II)
CC   or agonist of (I) is useful for treating or preventing a disorder
CC   associated with decreased expression or activity of GAPN, and an
CC   antagonist of (I) is useful for treating or preventing a disorder
CC   associated with increased expression or activity of GAPN (all claimed).
CC   (I) is useful as immunogen to raise antibodies that specifically
CC   recognize GAPN proteins. (II) is useful to drive in vivo expression of
CC   GAPN proteins, and as hybridization probes to detect, characterize and
CC   quantify GAPN nucleic acids in and isolate GAPN nucleic acids from both
CC   genomic and transcript-derived nucleic acid samples. This sequence
CC   represents a 17-mer oligonucleotide spanning the GAP_N DNA sequence.
XX
SQ   Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 CTGCGGGTGACCGAG 29
              ||||||||||  || |
Db         16 CTGCGGGTGAGCGTG 2


RESULT 1112
ADD20929/c
ID   ADD20929 standard; DNA; 17 BP.
XX
AC   ADD20929;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human GAP_N DNA 17-mer oligo #161.
XX
KW   gene therapy; antibody therapy; modulator of GAPN;
KW   GTP-activator for Rab-like GTPase; GAP_N; immunogen; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003033703-A2.
XX
PD   24-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032597.
XX
PR   15-OCT-2001; 2001US-0330323P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-403224/38.
XX
PT   Novel human GTP-activator protein for Rab-like GTPase and polynucleotide
PT   encoding the protein, useful for diagnosing, treating or preventing
PT   disorders associated with increased expression or activity of the
PT   protein.
XX
PS   Example 2; SEQ ID NO 185; 149pp; English.
XX
CC   The invention relates to an isolated human GTP-activator protein for Rab-
CC   like GTPase (GAPN) polypeptide (I), a sequence having 65% identity to
CC   (I), a sequence in which at least 95% of deviations from (I) are
CC   conservative substitutions, or a fragment of at least 8 contiguous amino
CC   acids of (I). The polypeptide is useful for identifying a specific
CC   binding partner for itself, by contacting the polypeptide in vivo to a
CC   potential binding partner and determining if the polypeptide binding
CC   partner binds to the polypeptide. (I) and a nucleic acid encoding the
CC   polypeptide (II) are useful for diagnosing or monitoring a disease caused
CC   by altered expression of GAPN, by determining the level of expression of
CC   GAPN in a sample of nucleic acids or proteins that derives from a subject
CC   suspected to have the disease, alterations from a normal level of
CC   expression providing diagnostic and/or monitoring information. (I), (II)
CC   or agonist of (I) is useful for treating or preventing a disorder
CC   associated with decreased expression or activity of GAPN, and an
CC   antagonist of (I) is useful for treating or preventing a disorder
CC   associated with increased expression or activity of GAPN (all claimed).
CC   (I) is useful as immunogen to raise antibodies that specifically
CC   recognize GAPN proteins. (II) is useful to drive in vivo expression of
CC   GAPN proteins, and as hybridization probes to detect, characterize and
CC   quantify GAPN nucleic acids in and isolate GAPN nucleic acids from both
CC   genomic and transcript-derived nucleic acid samples. This sequence
CC   represents a 17-mer oligonucleotide spanning the GAP_N DNA sequence.
XX
SQ   Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 CTGCGGGTGACCGAG 29
              ||||||||||  || |
Db         17 CTGCGGGTGAGCGTG 3


RESULT 1113
ADD20888
ID   ADD20888 standard; DNA; 17 BP.
XX
AC   ADD20888;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human GAP_N DNA 17-mer oligo #120.
XX
KW   gene therapy; antibody therapy; modulator of GAPN;
```

KW GTP-activator for Rab-like GTPase; GAP_N; immunogen; ss.
XX
OS Homo sapiens.
XX
PN WO2003033703-A2.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032597.
XX
PR 15-OCT-2001; 2001US-0330323P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-403224/38.
XX
PT Novel human GTP-activator protein for Rab-like GTPase and polynucleotide
PT encoding the protein, useful for diagnosing, treating or preventing
PT disorders associated with increased expression or activity of the
PT protein.
XX
PS Example 2; SEQ ID NO 144; 149pp; English.
XX
CC The invention relates to an isolated human GTP-activator protein for Rab-
CC like GTPase (GAPN) polypeptide (I), a sequence having 65% identity to
CC (I), a sequence in which at least 95% of deviations from (I) are
CC conservative substitutions, or a fragment of at least 8 contiguous amino
CC acids of (I). The polypeptide is useful for identifying a specific
CC binding partner for itself, by contacting the polypeptide in vivo to a
CC potential binding partner and determining if the polypeptide binding
CC partner binds to the polypeptide. (I) and a nucleic acid encoding the
CC polypeptide (II) are useful for diagnosing or monitoring a disease caused
CC by altered expression of GAPN, by determining the level of expression of
CC GAPN in a sample of nucleic acids or proteins that derives from a subject
CC suspected to have the disease, alterations from a normal level of
CC expression providing diagnostic and/or monitoring information. (I), (II)
CC or agonist of (I) is useful for treating or preventing a disorder
CC associated with decreased expression or activity of GAPN, and an
CC antagonist of (I) is useful for treating or preventing a disorder
CC associated with increased expression or activity of GAPN (all claimed).
CC (I) is useful as immunogen to raise antibodies that specifically
CC recognize GAPN proteins. (II) is useful to drive in vivo expression of
CC GAPN proteins, and as hybridization probes to detect, characterize and
CC quantify GAPN nucleic acids in and isolate GAPN nucleic acids from both
CC genomic and transcript-derived nucleic acid samples. This sequence
CC represents a 17-mer oligonucleotide spanning the GAP_N DNA sequence.
XX
SQ Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

```
  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        383 CGACGACGGCGCCAA 397
              ||||||| |||| |
Db          2 CGACGACGCCGCCTA 16
```

RESULT 1114
ADD20931/c
ID ADD20931 standard; DNA; 17 BP.
XX
AC ADD20931;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human GAP_N DNA 17-mer oligo #163.
XX
KW gene therapy; antibody therapy; modulator of GAPN;
KW GTP-activator for Rab-like GTPase; GAP_N; immunogen; ss.
XX
OS Homo sapiens.
XX
PN WO2003033703-A2.
XX
PD 24-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032597.
XX
PR 15-OCT-2001; 2001US-0330323P.
XX
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-403224/38.
XX
PT Novel human GTP-activator protein for Rab-like GTPase and polynucleotide
PT encoding the protein, useful for diagnosing, treating or preventing
PT disorders associated with increased expression or activity of the
PT protein.
XX
PS Example 2; SEQ ID NO 187; 149pp; English.
XX
CC The invention relates to an isolated human GTP-activator protein for Rab-
CC like GTPase (GAPN) polypeptide (I), a sequence having 65% identity to
CC (I), a sequence in which at least 95% of deviations from (I) are
CC conservative substitutions, or a fragment of at least 8 contiguous amino
CC acids of (I). The polypeptide is useful for identifying a specific
CC binding partner for itself, by contacting the polypeptide in vivo to a
CC potential binding partner and determining if the polypeptide binding
CC partner binds to the polypeptide. (I) and a nucleic acid encoding the
CC polypeptide (II) are useful for diagnosing or monitoring a disease caused
CC by altered expression of GAPN, by determining the level of expression of
CC GAPN in a sample of nucleic acids or proteins that derives from a subject
CC suspected to have the disease, alterations from a normal level of
CC expression providing diagnostic and/or monitoring information. (I), (II)
CC or agonist of (I) is useful for treating or preventing a disorder
CC associated with decreased expression or activity of GAPN, and an
CC antagonist of (I) is useful for treating or preventing a disorder
CC associated with increased expression or activity of GAPN (all claimed).
CC (I) is useful as immunogen to raise antibodies that specifically
CC recognize GAPN proteins. (II) is useful to drive in vivo expression of
CC GAPN proteins, and as hybridization probes to detect, characterize and
CC quantify GAPN nucleic acids in and isolate GAPN nucleic acids from both
CC genomic and transcript-derived nucleic acid samples. This sequence
CC represents a 17-mer oligonucleotide spanning the GAP_N DNA sequence.
XX
SQ Sequence 17 BP; 3 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

```
  Query Match             2.8%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 CTGCGGGTGACCGAG 29
              |||||||||| || |
Db         15 CTGCGGGTGAGCGTG 1
```

RESULT 1115
AAQ26549
ID AAQ26549 standard; DNA; 18 BP.
XX
AC AAQ26549;
XX
DT 08-JAN-1993 (first entry)
XX
DE Control probe #4 for caucosoid RING11 gene.
XX
KW immunosuppressants; immunoenhancers; treatment; diagnosis; screening;
KW immune disorders; transporter peptides; proteasome complex;
KW MHC class I molecules; HLA; antigen processing; antigen presentation;
KW autoimmune disease; ankylosing spondylitus; prenatal diagnosis;
KW polymerase chain reaction; ss.

```
XX
OS   Synthetic.
XX
PN   WO9211289-A1.
XX
PD   09-JUL-1992.
XX
PF   19-DEC-1991;   91WO-GB002278.
XX
PR   19-DEC-1990;   90GB-00027520.
PR   16-SEP-1991;   91GB-00019711.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI   Trowsdale J,  Kelly AP,  Glynne R,  Powis SH;
XX
DR   WPI; 1992-250030/30.
XX
PT   DNA encoding RING4, RING10, RING11 AND RING12 proteins - for treatment
PT   and diagnosis of immune disorders and screening of new immunosuppressants
PT   and immuno:enhancers.
XX
PS   Example 2; Page 40; 101pp; English.
XX
CC   This probe was used together with AAQ26546-51 to analyse caucosoid
CC   controls by oligonucleotide typing, whilst investigating RING 11
CC   polymorphisms - see AAQ26544,5
XX
SQ   Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        267 CACCTGGAGCAGGGC 281
              | ||||||||| ||||
Db          2 CTCCTGGAGCTGGGC 16


RESULT 1116
AAQ42271
ID   AAQ42271 standard; cDNA; 18 BP.
XX
AC   AAQ42271;
XX
DT   25-MAR-2003  (revised)
DT   13-SEP-1993  (first entry)
XX
DE   PCR primer KBA-gamma2 to amplify 3'-end (constant region) of Fd.
XX
KW   Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW   autoimmune disease; cell killing; toxin;
KW   overlap extension polymerase chain reaction; rabbit muscle aldolase; ss.
XX
OS   Synthetic.
XX
PN   WO9309130-A1.
XX
PD   13-MAY-1993.
XX
PF   04-NOV-1992;   92WO-US009487.
XX
PR   04-NOV-1991;   91US-00787567.
PR   19-JUN-1992;   92US-00901707.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Berhard SL,  Better MD,  Carroll SF,  Lane JA,  Lei SP;
XX
DR   WPI; 1993-167617/20.
XX
PT   Analogues of type I ribosome inactivating protein - useful as cytotoxic
PT   agents, immuno toxins for treating auto immune diseases, cancer, graft
PT   versus host disease and selective cell killing in=vivo.
XX
PS   Example 10; Page 67; 163pp; English.
XX
CC   A gelonin gene fusion to the 3'-end of the H65 Fd chain with the 21 amino
CC   acid rabbit muscle aldolase (RMA) linker sequence (20 amino acids from
CC   RMA, plus 1 amino acid introduced to facilitate cloning) was assembled in
CC   a three piece ligation. Primers KBA-gamma2 and RMAG-1 (AAQ42271 and
CC   AAQ42272, respectively) were used to amplify the 3'-end (constant region)
CC   of the Fd gene from a source plasmid. (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 18 BP; 2 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        344 CCGGCTGCTCTACAG 358
              ||||||| ||||||
Db          3 CCGGCTGTCCTACAG 17


RESULT 1117
AAQ34632
ID   AAQ34632 standard; cDNA; 18 BP.
XX
AC   AAQ34632;
XX
DT   25-MAR-2003  (revised)
DT   10-MAY-1993  (first entry)
XX
DE   Human bcr-abl junction mRNA transcript antisense oligonucleotide.
XX
KW   Leukaemia; treatment; blast crisis; specific; CML; translocation;
KW   Philadelphia chromosome; chronic myeloid; chronic myelogenous; leukemia;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9222303-A1.
XX
PD   23-DEC-1992.
XX
PF   15-JUN-1992;   92WO-US005035.
XX
PR   18-JUN-1991;   91US-00718302.
PR   14-APR-1992;   92US-00869911.
XX
PA   (UTEM ) UNIV TEMPLE.
XX
PI   Calabretta B,  Gewirtz AM;
XX
DR   WPI; 1993-017893/02.
XX
PT   Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT   nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT   without adversely affecting normal haematopoiesis.
XX
PS   Disclosure; Page 51; 74pp; English.
XX
CC   The sequence is that of an antisense oligonucleotide complementary (with
CC   two mismatches) to a target sequence of the bcr-abl mRNA transcript
CC   AAQ34631, which includes the bcr-abl translocation junction and not more
CC   than about 13 nucleotides of the abl-derived portion of the transcript.
CC   It is used as part of a method to treat leukaemias characterised by the
CC   Philadelphia chromosome translocation. It is highly selective and patient
CC   specific unlike conventional chemotherapy, which affects non-malignant
CC   cells. Dosage selection is thus less critical than with conventional
CC   treatment. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 2 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
```

```
  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        398 GAAGGTCTTCTACGT 412
              | ||| |||||||||
Db          1 GCAGGGCTTCTACGT 15


RESULT 1118
AAQ34633
ID   AAQ34633 standard; cDNA; 18 BP.
XX
AC   AAQ34633;
XX
DT   25-MAR-2003  (revised)
DT   10-MAY-1993  (first entry)
XX
DE   Human bcr-abl junction mRNA transcript antisense oligonucleotide.
XX
KW   Leukaemia; treatment; blast crisis; specific; CML; translocation;
KW   Philadelphia chromosome; chronic myeloid; chronic myelogenous; leukemia;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9222303-A1.
XX
PD   23-DEC-1992.
XX
PF   15-JUN-1992;   92WO-US005035.
XX
PR   18-JUN-1991;   91US-00718302.
PR   14-APR-1992;   92US-00869911.
XX
PA   (UTEM ) UNIV TEMPLE.
XX
PI   Calabretta B,  Gewirtz AM;
XX
DR   WPI; 1993-017893/02.
XX
PT   Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT   nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT   without adversely affecting normal haematopoiesis.
XX
PS   Disclosure; Page 51; 74pp; English.
XX
CC   The sequence is that of an antisense oligonucleotide complementary to a
CC   target sequence of the bcr-abl mRNA transcript AAQ34631, which includes
CC   the bcr-abl translocation junction and not more than about 13 nucleotides
CC   of the abl-derived portion of the transcript. It is used as part of a
CC   method to treat leukaemias characterised by the Philadelphia chromosome
CC   translocation. It is highly selective and patient specific unlike
CC   conventional chemotherapy, which affects non-malignant cells. Dosage
CC   selection is thus less critical than with conventional treatment.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        398 GAAGGTCTTCTACGT 412
              ||||| ||||| |||
Db          1 GAAGGGCTTCTGCGT 15


RESULT 1119
AAQ34638/c
ID   AAQ34638 standard; cDNA; 18 BP.
XX
AC   AAQ34638;
XX
DT   25-MAR-2003  (revised)
DT   10-MAY-1993  (first entry)
XX
DE   Human b1a2 breakpoint sequence.
XX
KW   Leukaemia; treatment; blast crisis; specific; CML; translocation;
KW   Philadelphia chromosome; chronic myeloid; chronic myelogenous; leukemia;
KW   bcr; abl; ss.
XX
OS   Synthetic.
XX
PN   WO9222303-A1.
XX
PD   23-DEC-1992.
XX
PF   15-JUN-1992;   92WO-US005035.
XX
PR   18-JUN-1991;   91US-00718302.
PR   14-APR-1992;   92US-00869911.
XX
PA   (UTEM ) UNIV TEMPLE.
XX
PI   Calabretta B,  Gewirtz AM;
XX
DR   WPI; 1993-017893/02.
XX
PT   Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT   nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT   without adversely affecting normal haematopoiesis.
XX
PS   Example; Page 38; 74pp; English.
XX
CC   The sequence is that of the breakpoint junction from RNA isolated from
CC   cell line ALL-1 derived from a Ph1-positive ALL patient (Erikson et al.
CC   1986). The junction sequence was used in the prepn. of antisense
CC   oligonucleotides which can be used as part of a method to treat
CC   leukaemias characterised by the Philadelphia chromosome translocation.
CC   This method is highly selective and patient specific unlike conventional
CC   chemotherapy, which affects non-malignant cells. Dosage selection is thus
CC   less critical than with conventional treatment. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        398 GAAGGTCTTCTACGT 412
              ||||| ||||| |||
Db         18 GAAGGGCTTCTGCGT 4


RESULT 1120
AAQ64697
ID   AAQ64697 standard; DNA; 18 BP.
XX
AC   AAQ64697;
XX
DT   25-MAR-2003  (revised)
DT   03-JAN-1995  (first entry)
XX
DE   b1a2 junction antisense oligonucleotide.
XX
KW   Translocation; bcr-abl; b2a2; L-6; b3a2; K-28; b1a2; proliferation;
KW   neoplastic cell; cancer; tumour; proto-oncogene; antisense;
KW   oligonucleotide; chronic myelogenous leukemia; CML;
KW   acute lymphocytic leukemia; ALL; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
```

```
FT   misc_feature    9. .10
FT                   /*tag=  a
FT                   /note= "breakpoint"
XX
PN   WO9408625-A1.
XX
PD   28-APR-1994.
XX
PF   10-AUG-1993;   93WO-US007541.
XX
PR   21-OCT-1992;   92US-00965671.
XX
PA   (UTEM ) UNIV TEMPLE.
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Calabretta B,  Skorski T;
XX
DR   WPI; 1994-150955/18.
XX
PT   Inhibiting proliferation of neoplastic cells - by using oncogene or proto
PT   -oncogene anti-sense oligo:nucleotide and non-oligo:nucleotide
PT   chemotherapeutic agent.
XX
PS   Disclosure; Page 48; 110pp; English.
XX
CC   The bcr-abl antisense oligonucleotide is complementary to a position of
CC   the bcr-abl mRNA corresp. to the breakpoint junction between the bcr-
CC   derived and abl-derived portions of the mRNA. Most pref. antisense
CC   oligonucleotides complementary to the b2a2 junction includes the
CC   sequences given in AAQ64681-87. Most pref. antisense oligonucleotides
CC   complementary to the b3a2 junction includes the sequences given in
CC   AAQ64688-94. Most pref. antisense oligonucleotides complementary to the
CC   b1a2 junction includes the sequences given in AAQ64695-701. (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        398 GAAGGTCTTCTACGT 412
              ||||| ||||| |||
Db          1 GAAGGGCTTCTGCGT 15


RESULT 1121
AAQ57173
ID   AAQ57173 standard; mRNA; 18 BP.
XX
AC   AAQ57173;
XX
DT   25-MAR-2003  (revised)
DT   26-JUL-1994  (first entry)
XX
DE   Enzymatic RNA molecule TNF-alpha mRNA target sequence.
XX
KW   Tumour necrosis factor; specific; cleavage; target RNA; protein;
KW   expression; inhibitor; inhibition; ribozyme; treatment; prophylaxis;
KW   prevention; psoriasis; asthma; inflammatory diseases; restenosis;
KW   cardiovascular condition; hypertension; arthritis; ss.
XX
OS   Synthetic.
XX
PN   WO9402595-A1.
XX
PD   03-FEB-1994.
XX
PF   02-JUL-1993;   93WO-US006316.
XX
PR   17-JUL-1992;   92US-00916763.
PR   07-DEC-1992;   92US-00987132.
PR   07-DEC-1992;   92US-00989848.
PR   07-DEC-1992;   92US-00989849.
PR   19-JAN-1993;   93US-00008895.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Sullivan SM,  Draper KG;
XX
DR   WPI; 1994-048853/06.
XX
PT   Enzymatic RNA molecules which cleave mRNA - used to treat or prevent
PT   inflammatory, arthritic, stenotic or cardiovascular diseases or
PT   conditions.
XX
PS   Claim 3; Page 16; 65pp; English.
XX
CC   This is a TNF-alpha mRNA target sequence (nucleotide no. 1084) of an
CC   enzymatic RNA molecule (ribozyme) which cleaves mRNA associated with the
CC   development or maintenance of a psoriatic or asthmatic condition. The
CC   concn. of the ribozyme necessary to effect a therapeutic treatment is
CC   lower than that of an antisense oligonucleotide and the specificity of
CC   action is higher. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 7 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         44 TGGCCACCACTCAGA 58
              |||| |||||| |||
Db          2 TGGCAACCACTAAGA 16


RESULT 1122
AAQ76140
ID   AAQ76140 standard; DNA; 18 BP.
XX
AC   AAQ76140;
XX
DT   25-MAR-2003  (revised)
DT   28-JUL-1995  (first entry)
XX
DE   Fd gene 3' (constant region) PCR primer KBA-gamma2.
XX
KW   Gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer;
KW   graft-versus-host disease; PCR primer; Fd gene; ss.
XX
OS   Synthetic.
XX
PN   WO9426910-A1.
XX
PD   24-NOV-1994.
XX
PF   12-MAY-1994;   94WO-US005348.
XX
PR   12-MAY-1993;   93US-00064691.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Better MD,  Carroll SF,  Studnicka GM;
XX
DR   WPI; 1995-006804/01.
XX
PT   Polynucleotide(s) encoding type I ribosome-inactivating proteins - which
PT   are suitable for use as components of cytotoxic therapeutic agents.
XX
PS   Example 14; Page 93; 221pp; English.
XX
CC   AAQ76140 and AAQ76141 are a pair of primers for the PCR amplification of
CC   the Fd gene 3' (constant region), they were used in the construction of a
CC   Fd::RMA linker::gelonin cytotoxic therapeutic agent (CTA),
CC   immunoconjugate. CTAs can be used in the treatment of diseases where the
CC   elimination of a particular cell type is desired, such as autoimmune
```

```
CC   disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 18 BP; 2 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        344 CCGGCTGCTCTACAG 358
              ||||||| ||||||
Db          3 CCGGCTGTCCTACAG 17


RESULT 1123
AAQ87648/c
ID   AAQ87648 standard; DNA; 18 BP.
XX
AC   AAQ87648;
XX
DT   19-DEC-1995  (first entry)
XX
DE   Chick antisense oligonucleotide to p75 NGFR gene.
XX
KW   Oligonucleotide; antisense; down-regulation; expression; trauma;
KW   nerve growth factor receptor; neurodegenerative disease; Alzheimer's;
KW   Parkinson's; Hungtington's disease; multiple sclerosis;
KW   vascular ischaemia; stroke; ss.
XX
OS   Synthetic.
XX
PN   WO9511253-A1.
XX
PD   27-APR-1995.
XX
PF   18-OCT-1994;   94WO-AU000631.
XX
PR   18-OCT-1993;   93AU-00001870.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Barrett GL;
XX
DR   WPI; 1995-170186/22.
XX
PT   Anti:sense oligo:nucleotide(s) to nerve growth factor receptor gene - of
PT   p75 NGFR, down-regulate expression and enhance neurone survival; for
PT   treating cerebal palsy, Alzheimer's disease, stroke, etc.
XX
PS   Example 3; Page 35; 59pp; English.
XX
CC   The sequence of an antisense oligonucleotide to the chick nerve growth
CC   factor receptor (NGFR) gene which was used as a control for the survival
CC   of mouse dorsal root ganglial (DRG) cells treated with oligonucleotides
CC   AAQ87641-2. These oligonucleotides are antisense sequences directed at
CC   down-regulating the expression of the gene encoding the mouse p75 NGFR
CC   gene. The oligonucleotides can be used in methods to treat
CC   neurodegenerative conditions associated with disease and/or trauma such
CC   as Alzheimer's, Parkinson's or Hungtington's disease, multiple sclerosis,
CC   vascular ischaemia associated with stroke, etc
XX
SQ   Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        169 TGTACTACGAGTCCA 183
              ||||| ||||||||
Db         17 TGTACAGCGAGTCCA 3


RESULT 1124
AAQ92348
ID   AAQ92348 standard; DNA; 18 BP.
XX
AC   AAQ92348;
XX
DT   25-MAR-2003  (revised)
DT   01-JAN-1996  (first entry)
XX
DE   PCR primer KBA-gamma2 for linking RMA linker with Fd gene.
XX
KW   RMA linker segment; Fd; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5416202-A.
XX
PD   16-MAY-1995.
XX
PF   09-DEC-1992;   92US-00988430.
XX
PR   04-NOV-1991;   91US-00787567.
PR   19-JUN-1992;   92US-00901707.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Lei S,  Carroll SF,  Lane JA,  Bernhard SL,  Better MD;
XX
DR   WPI; 1995-193480/25.
XX
PT   Polynucleotide(s) encoding gelonin analogues - having a cysteine residue
PT   for intermolecular bonding for the prodn. of immuno-toxin(s).
XX
PS   Example; Col 41; 66pp; English.
XX
CC   Plasmid pSH4 contains an Fd gene linked in frame to the RMA linker
CC   sequence. The RMA gene segment was linked to the 3'-end of Fd by overlap
CC   extension PCR as follows. The 3'-end (constant region) of the Fd gene was
CC   amplified by PCR from a source plasmid with the primers KBA-gamma2 and
CC   RMAP-1. The product of this reaction was mixed with primer RMA-76, which
CC   annealed to the amplified product of the first reaction, and the mixture
CC   was amplified with primers KBA-gamma2 and RMAK-2. (Updated on 25-MAR-2003
CC   to correct PR field.)
XX
SQ   Sequence 18 BP; 2 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        344 CCGGCTGCTCTACAG 358
              ||||||| ||||||
Db          3 CCGGCTGTCCTACAG 17


RESULT 1125
AAT28318/c
ID   AAT28318 standard; DNA; 18 BP.
XX
AC   AAT28318;
XX
DT   19-NOV-1996  (first entry)
XX
DE   Multi-G oligonucleotide rb SCR (random).
XX
KW   Multi-G oligonucleotide; antisense sequence; c-myb; nuclease resistant;
KW   phosphorothioate linkage; phosphorodithioate linkage; inhibitor; therapy;
KW   cell proliferation; smooth muscle cell; proliferation protein;
KW   vascular restenosis; arterial restenosis; ss.
XX
OS   Synthetic.
XX
PN   WO9611266-A2.
XX
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PD   18-APR-1996.
XX
PF   03-OCT-1995;   95WO-US012770.
XX
PR   05-OCT-1994;   94US-00318458.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Burgess TL,  Farrell CL,  Fisher EF;
XX
DR   WPI; 1996-209848/21.
XX
PT   New modified oligo:nucleotide(s) contg. consecutive guanine residues -
PT   inhibit proliferation of smooth muscle cells, esp. to prevent arterial
PT   restenosis.
XX
PS   Example 1; Page 41; 67pp; English.
XX
CC   AAT28317-T28347 represent multi-G oligonucleotides. AAT28317-T28324 are
CC   based on an antisense sequence against the c-myb target. These sequences
CC   are oligonucleotides of the invention. These sequences can be modified to
CC   become more nuclease resistant, using phosphorothioate,
CC   phosphorodithioate, or 3'-carbon modified links. To screen for modified
CC   multi-G sequences that inhibit cell proliferation, cultured smooth muscle
CC   cells that are arrested in the G0 phase, are induced to proliferate in
CC   the presence of the multi-G sequence. The cultured smooth muscle cells
CC   used in this method are attached to a solid support, and growth arrest is
CC   achieved on a starvation medium, followed by transfer to a normal growth
CC   medium to induce proliferation. The compounds that provide over 50%
CC   inhibition at a set dosage are selected as being useful for inhibiting
CC   vascular restenosis. The multi-G oligonucleotides are used to inhibit
CC   proliferation of smooth muscle cells, such as to prevent arterial
CC   restenosis. These sequences are not antisense sequences, but are thought
CC   to work in a similar way. The sequences are thought to act by binding to
CC   proteins involved in the proliferation process. Compounds containing
CC   these multi-G oligonucleotides are not toxic, and their effect on cell
CC   proliferation is fully reversible
XX
SQ   Sequence 18 BP; 0 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        379 ACCGCGACGACGGCG 393
              |||||  ||||||||
Db         15 ACCGCCGCGACGGCG 1


RESULT 1126
AAT60160/c
ID   AAT60160 standard; DNA; 18 BP.
XX
AC   AAT60160;
XX
DT   01-DEC-1997  (first entry)
XX
DE   Collagen gene promoter region binding oligomer Oligo 164 APS.
XX
KW   Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
KW   myocardial fibrosis; hypertensive heart disease; atherosclerosis;
KW   restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
KW   hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .18
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages"
XX
PN   WO9710254-A1.
XX
PD   20-MAR-1997.
XX
PF   12-SEP-1996;   96WO-US014640.
XX
PR   15-SEP-1995;   95US-00528836.
PR   11-SEP-1996;   96US-00712357.
XX
PA   (GUNT/) GUNTAKA R V.
XX
PI   Guntaka RV,  Weber KT,  Kovacs A,  Kandala J;
XX
DR   WPI; 1997-202172/18.
XX
PT   Triplex forming oligomer binds to collagen gene promoter region - used to
PT   impede pathological fibrosis etc.
XX
PS   Claim 18; Page 36; 52pp; English.
XX
CC   An oligomer has been produced which is capable of inhibiting expression
CC   of a collagen gene. The present sequence represents a specifically
CC   claimed oligomer Oligo 164 APS, which binds to the polypurine-
CC   polypyrimidine region of the rat alpha1(I) collagen gene promoter region.
CC   The oligomer may be used to impede pathological fibrosis which is
CC   associated with myocardial fibrosis in hypertensive heart diseases,
CC   atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
CC   fibrosis found in scleroderma, in hypertrophic scars and in skin
CC   following burn injury. The oligomer inhibits expression of a collagen
CC   gene after insertion into a cell by causing an intracellular reaction
CC   which inhibits gene expression. The oligomer is preferably a triplex
CC   forming oligomer (TFO) which is targeted to a 30-mer polypurine
CC   oligonucleotide corresponding to the noncoding strand of the promoter
CC   between -170 and -140. This section was chosen due to its binding
CC   stability at physiological pH
XX
SQ   Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 CTTCCTCACTTTCCT 376
              | ||||| |||||||
Db         18 CCTCCTCCCTTTCCT 4


RESULT 1127
AAT60165/c
ID   AAT60165 standard; DNA; 18 BP.
XX
AC   AAT60165;
XX
DT   01-DEC-1997  (first entry)
XX
DE   Collagen gene promoter region binding oligomer Oligo 164 AP.
XX
KW   Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
KW   myocardial fibrosis; hypertensive heart disease; atherosclerosis;
KW   restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
KW   hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
XX
OS   Synthetic.
XX
PN   WO9710254-A1.
XX
PD   20-MAR-1997.
XX
PF   12-SEP-1996;   96WO-US014640.
XX
PR   15-SEP-1995;   95US-00528836.
PR   11-SEP-1996;   96US-00712357.
XX
PA   (GUNT/) GUNTAKA R V.
XX
```

PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX
DR WPI; 1997-202172/18.
XX
PT Triplex forming oligomer binds to collagen gene promoter region - used to
PT impede pathological fibrosis etc.
XX
PS Example 4; Page 35; 52pp; English.
XX
CC An oligomer has been produced which is capable of inhibiting expression
CC of a collagen gene. The present sequence represents an oligomer Oligo 164
CC AP, which binds to the polypurine-polypyrimidine region of the rat
CC alpha1(I) collagen gene promoter region. The oligomer may be used to
CC impede pathological fibrosis which is associated with myocardial fibrosis
CC in hypertensive heart diseases, atherosclerosis, restenosis, liver
CC cirrhosis, lung fibrosis, and skin fibrosis found in scleroderma, in
CC hypertrophic scars and in skin following burn injury. The oligomer
CC inhibits expression of a collagen gene after insertion into a cell by
CC causing an intracellular reaction which inhibits gene expression. The
CC oligomer is preferably a triplex forming oligomer (TFO) which is targeted
CC to a 30-mer polypurine oligonucleotide corresponding to the noncoding
CC strand of the promoter between -170 and -140. This section was chosen due
CC to its binding stability at physiological pH
XX
SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 362 CTTCCTCACTTTCCT 376
| ||||| |||||||
Db 18 CCTCCTCCCTTTCCT 4

RESULT 1128
AAT60158/c
ID AAT60158 standard; DNA; 18 BP.
XX
AC AAT60158;
XX
DT 01-DEC-1997 (first entry)
XX
DE Collagen gene promoter region binding oligomer Oligo 147 P.
XX
KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
XX
OS Synthetic.
XX
PN WO9710254-A1.
XX
PD 20-MAR-1997.
XX
PF 12-SEP-1996; 96WO-US014640.
XX
PR 15-SEP-1995; 95US-00528836.
PR 11-SEP-1996; 96US-00712357.
XX
PA (GUNT/) GUNTAKA R V.
XX
PI Guntaka RV, Weber KT, Kovacs A, Kandala J;
XX
DR WPI; 1997-202172/18.
XX
PT Triplex forming oligomer binds to collagen gene promoter region - used to
PT impede pathological fibrosis etc.
XX
PS Claim 18; Page 34; 52pp; English.
XX
CC An oligomer has been produced which is capable of inhibiting expression
CC of a collagen gene. The present sequence represents a specifically
CC claimed oligomer Oligo 147 P, which binds to the polypurine-
CC polypyrimidine region of the rat alpha1(I) collagen gene promoter region.
CC The oligomer may be used to impede pathological fibrosis which is
CC associated with myocardial fibrosis in hypertensive heart diseases,
CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
CC fibrosis found in scleroderma, in hypertrophic scars and in skin
CC following burn injury. The oligomer inhibits expression of a collagen
CC gene after insertion into a cell by causing an intracellular reaction
CC which inhibits gene expression. The oligomer is preferably a triplex
CC forming oligomer (TFO) which is targeted to a 30-mer polypurine
CC oligonucleotide corresponding to the noncoding strand of the promoter
CC between -170 and -140. This section was chosen due to its binding
CC stability at physiological pH
XX
SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 362 CTTCCTCACTTTCCT 376
| ||||| |||||||
Db 18 CCTCCTCCCTTTCCT 4

RESULT 1129
AAT61597/c
ID AAT61597 standard; DNA; 18 BP.
XX
AC AAT61597;
XX
DT 22-OCT-1997 (first entry)
XX
DE Humicola lanuginosa lipase gene fragment PCR primer 4699.
XX
KW Lipase; polypeptide variant; in vivo recombination; shuffling;
KW Saccharomyces cerevisiae; Humicola lanuginosa; detergent;
KW polymerase chain reaction; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9707205-A1.
XX
PD 27-FEB-1997.
XX
PF 12-AUG-1996; 96WO-DK000343.
XX
PR 11-AUG-1995; 95DK-00000907.
PR 20-SEP-1995; 95DK-00001047.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Okkels JS;
XX
DR WPI; 1997-165289/15.
XX
PT Preparing polypeptide variants with improved functional properties - by
PT in vivo recombination between opened plasmid and homologous DNA, to
PT produce e.g. enzymes with improved washing and dishwashing properties.
XX
PS Example 3; Page 41; 68pp; English.
XX
CC PCR primers (AAT61596-604) are used to amplify fragments of the Humicola
CC lanuginosa lipase gene coding sequence (see also AAT61593). For example,
CC primer 4699 (AAT61597) can be used with primer 5164 (AAT61598) to make a
CC 900 bp fragment. The lipase gene fragments are used in an improved method
CC of preparing positive polypeptide variants (see also AAW13557-58). This
CC involves shuffling opened plasmid and homologous DNA sequences in an
CC iterative in vivo recombination system using a eukaryotic cell (such as
CC yeast) as a recombination host cell
XX
SQ Sequence 18 BP; 3 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

```
  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        305 GAGCCCCGGGGACCG 319
              || ||||||| ||||
Db         15 GATCCCCGGGTACCG 1


RESULT 1130
AAT61608/c
ID   AAT61608 standard; DNA; 18 BP.
XX
AC   AAT61608;
XX
DT   22-OCT-1997  (first entry)
XX
DE   Humicola lanuginosa lipase gene fragment PCR primer 4699.
XX
KW   Lipase; polypeptide variant; in vivo recombination; shuffling;
KW   Saccharomyces cerevisiae; Humicola lanuginosa; detergent;
KW   polymerase chain reaction; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9707206-A1.
XX
PD   27-FEB-1997.
XX
PF   12-AUG-1996;   96WO-DK000344.
XX
PR   11-AUG-1995;   95DK-00000907.
PR   20-SEP-1995;   95DK-00001047.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Okkels JS;
XX
DR   WPI; 1997-165290/15.
XX
PT   Preparing polypeptide variants with improved functional properties - by
PT   in vivo recombination between opened plasmid and homologous DNA, to
PT   produce e.g. enzymes with improved washing and dishwashing properties.
XX
PS   Example 3; Page 41; 68pp; English.
XX
CC   PCR primers (AAT61607-615) are used to amplify fragments of the Humicola
CC   lanuginosa lipase gene coding sequence (see also AAT61593). For example,
CC   primer 4699 (AAT61608) can be used with primer 5164 (AAT61609) to make a
CC   900 bp fragment. The lipase gene fragments are used in an improved method
CC   of preparing positive polypeptide variants (see also AAW13561-62). This
CC   involves shuffling opened plasmid and homologous DNA sequences in an
CC   iterative in vivo recombination system using a eukaryotic cell (such as
CC   yeast) as a recombination host cell
XX
SQ   Sequence 18 BP; 3 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        305 GAGCCCCGGGGACCG 319
              || ||||||| ||||
Db         15 GATCCCCGGGTACCG 1


RESULT 1131
AAV44606
ID   AAV44606 standard; DNA; 18 BP.
XX
AC   AAV44606;
XX
DT   24-NOV-1998  (first entry)
XX
DE   Human uncoupling protein-2 UCP2 gene reverse primer hUCP2g.e4r2.
XX
KW   Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
KW   obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
KW   hypothermia; wasting; cachexia; anorexia; inflammation; fever;
KW   hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9831396-A1.
XX
PD   23-JUL-1998.
XX
PF   22-APR-1997;   97WO-US006864.
XX
PR   15-JAN-1997;   97US-0034960P.
XX
PA   (UYDU-) UNIV DUKE.
PA   (REGC ) UNIV CALIFORNIA.
PA   (CNRS ) CENT NAT RECH SCI.
XX
PI   Surwit RS,  Collins SA,  Warden CH,  Seldin MF,  Ricquier D;
PI   Bouillaud F;
XX
DR   WPI; 1998-413823/35.
XX
PT   Method for treating disease associated with altered UCP-2 expression - by
PT   administering agent which enhances or inhibits UCP-2 activity,
PT   effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
PT   etc.
XX
PS   Example IX; Page 46; 98pp; English.
XX
CC   Primer hUCP2g.e4r2 is used with forward primer hUCPg.e4f2 (see AAV44605)
CC   in the PCR amplification of bp 1858-2281 in exon 4 of the human
CC   uncoupling protein-2 (UCP2) gene. Primers (see AAV44603-18) were designed
CC   to amplify hUCP2 exons 4, 6, 7 and 8 from genomic DNA. Common amino acid
CC   variants (see AAW69166) are present in exons 4, 6 and 8; A55V in exon 4,
CC   N190S in exon 6, and L294M in exon 8 (see also AAV44595). Restriction
CC   enzymes have been identified that would differentially digest each
CC   of the alleles. The invention relates to a method for treating disease
CC   associated with altered UCP2 expression, such as obesity, diabetes,
CC   syndrome X, hypothermia, hyperinsulinaemia, glucose intolerance, wasting,
CC   anorexia, inflammation, cachexia, fever or hyperthermia
XX
SQ   Sequence 18 BP; 4 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        330 GCGGACGACCAGGGC 344
              | ||| |||||||||
Db          4 GTGGAGGACCAGGGC 18


RESULT 1132
AAV46204
ID   AAV46204 standard; DNA; 18 BP.
XX
AC   AAV46204;
XX
DT   16-OCT-1998  (first entry)
XX
DE   Human HLA-A primer I1-214m.
XX
KW   Histocompatibility locus antigen; HLA-A class I; human; class typing;
KW   donor; host; tissue transplantation; primer; ss.
XX
OS   Synthetic.
```

```
OS   Homo sapiens.
XX
PN   WO9826091-A2.
XX
PD   18-JUN-1998.
XX
PF   12-DEC-1997;   97WO-CA000955.
XX
PR   12-DEC-1996;   96US-00766189.
XX
PA   (VISI-) VISIBLE GENETICS INC.
XX
PI   Blasczyk RH,  Leushner J;
XX
DR   WPI; 1998-348544/30.
XX
PT   HLA Class I typing - by primer-based amplification of target DNA using
PT   group-specific untranslated region primer pair.
XX
PS   Claim 4; Page 122; 185pp; English.
XX
CC   AAV46054 and AAV46200-V46264 are primers used in isolating human
CC   histocompatibility locus antigen (HLA-A) Class I alleles which are used
CC   in a novel method of HLA Class I typing. The method involves combining a
CC   group-specific untranslated region primer pair with a target DNA to allow
CC   primer-based amplification of the DNA, and determining whether a nucleic
CC   acid product is produced by the amplification. The ability of the primer
CC   pair to produce a product is associated with a particular HLA group type.
CC   The methods can be used for typing the 3 classical HLA Class I genes
CC   (comprising the loci HLA-A, HLA-B, and HLA-C) in e.g. donors and hosts
CC   for tissue transplantation. The initial group specific amplification
CC   allows a PCR based separation of haplotypes in 95% of patient samples.
CC   The subsequent sequencing can provide for high-resolution typing
XX
SQ   Sequence 18 BP; 2 A; 5 C; 10 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        138 CGCCTGGCGGTGGAG 152
              ||||||||||  || |
Db          1 CGCCTGGCGGGGGGG 15


RESULT 1133
AAV54355
ID   AAV54355 standard; DNA; 18 BP.
XX
AC   AAV54355;
XX
DT   15-JAN-1999  (first entry)
XX
DE   Human cell type PCR anchor primer K3.
XX
KW   Identification; gene expression; conserved motif; target; metastatic;
KW   non-metastatic; non-cancerous tissue; nucleic acid analysis; PCR primer;
KW   ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9839480-A1.
XX
PD   11-SEP-1998.
XX
PF   03-MAR-1998;   98WO-US004094.
XX
PR   03-MAR-1997;   97US-00785522.
XX
PA   (HAQQ/) HAQQI T M.
XX
PI   Haqqi TM;
XX
DR   WPI; 1998-506373/43.
XX
PT   Method of analysing nucleic acid in a sample - used for analysing
PT   expressed genes, and distinguishing between metastatic, non-metastatic
PT   and non-cancerous tissues.
XX
PS   Example 1; Page 24; 55pp; English.
XX
CC   A novel method has been developed of analysing a nucleic acid in a
CC   sample. The method comprises: (a) providing: (i) a sample containing
CC   nucleic acid; (ii) a first primer having a sequence of which at least a
CC   portion is at least partially complementary to a natural common non-
CC   coding sequence on a portion of the nucleic acid of the sample; (iii) a
CC   second primer having a sequence of which at least a portion is at least
CC   partially complementary to a restriction enzyme recognition sequence
CC   present on a portion of the nucleic acid of the sample; and (iv) a
CC   polymerase and polymerase chain reaction (PCR) reagents; (b) preparing
CC   the nucleic acid from the sample under conditions so as to produce
CC   amplifyable nucleic acid; (c) amplifying the nucleic acid with the first
CC   and second primers, the polymerase and the PCR reagents under conditions
CC   such that amplified product is generated; and (d) detecting the amplified
CC   product. The method can be used for analysing expressed genes in multiple
CC   samples, especially in human cancer cells. The method can also be used to
CC   distinguish between metastatic and non-metastatic cancer tissues as well
CC   as between normal and cancerous tissue. It can also be used to detect
CC   drug resistance. The method can also be used to classify and identify
CC   microorganisms. The present sequence represents a PCR anchor primer used
CC   in an example from the present invention
XX
SQ   Sequence 18 BP; 2 A; 7 C; 5 G; 2 T; 0 U; 2 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   72.2%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        250 CGGGCTCGGCCACGGTGC 267
              |||| || |||:|  |||
Db          1 CGGGATCCGCCRCNATGC 18


RESULT 1134
AAV35048
ID   AAV35048 standard; DNA; 18 BP.
XX
AC   AAV35048;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Hordeum vulgare MLO gene PCR primer.
XX
KW   Barley; MLO; mildew; pathogen; resistance; PCR primer; ss.
XX
OS   Synthetic.
OS   Hordeum vulgare.
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;   97WO-GB002046.
XX
PR   29-JUL-1996;   96GB-00015879.
PR   30-OCT-1996;   96GB-00022626.
PR   07-MAR-1997;   97GB-00004789.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Schulzelefert PMJ,  Panstruga R,  Bueschges R;
XX
DR   WPI; 1998-159149/14.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
```

```
PT   production of transgenic plants which have increased pathogen resistance.
XX
PS   Disclosure; Page 90; 150pp; English.
XX
CC   The sequence is that of a PCR primer used in the amplification of the MLO
CC   gene
XX
SQ   Sequence 18 BP; 1 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        147 GTGGAGGCCGGCTTC 161
              ||||||||||  |||
Db          3 GTGGAGGCCGTGTTC 17


RESULT 1135
AAV48537
ID   AAV48537 standard; DNA; 18 BP.
XX
AC   AAV48537;
XX
DT   15-OCT-1998  (first entry)
XX
DE   p53 gene antisense oligonucleotide p53-T-2.
XX
KW   p53; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP856579-A1.
XX
PD   05-AUG-1998.
XX
PF   31-JAN-1997;   97EP-00101531.
XX
PR   31-JAN-1997;   97EP-00101531.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Schlingensiepen K,  Brysch W;
XX
DR   WPI; 1998-400910/35.
XX
PT   Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT   consecutive guanosine or inosine - and have specific ratio of residues
PT   able to form two or three hydrogen bonds, have greater activity and
PT   reduced toxicity, used therapeutically or to modulate growth of cells in
PT   culture.
XX
PS   Example 2; Fig 4b; 286pp; English.
XX
CC   AAV48485-564 represent antisense oligonucleotides directed against the
CC   p53 gene. Of these, only oligonucleotides AAV48485-517 resulted in
CC   effective downregulation of negative growth by p53 and increased cell
CC   proliferation, while AAV48518-64 had little effect. The oligonucleotides
CC   exemplify the invention. The specification describes oligonucleotides
CC   that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC   can each form three hydrogen bonds to cytosine; do not contain four
CC   consecutive nucleotides able to form three H-bonds each to four
CC   consecutive cytosines; do not contain two sequences of three consecutive
CC   nucleotides each able to form three H-bonds to three consecutive
CC   cytosines, and the ratio between residues able to form two H-bonds each
CC   (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC   oligonucleotides are used to modulate expression of genes, particularly
CC   the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC   proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC   kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC   oligonucleotides can also be used to analyse function of proteins (by
CC   altering their expression or activity) and therapeutically, e.g. in cases
CC   of cancer or (targeting TGF) for stimulating the immune system
XX
SQ   Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         52 ACTCAGAGGAGTCTC 66
              |||||||| | |||
Db          4 ACTCAGAGGGGGCTC 18


RESULT 1136
AAV48422
ID   AAV48422 standard; DNA; 18 BP.
XX
AC   AAV48422;
XX
DT   15-OCT-1998  (first entry)
XX
DE   Transforming growth factor beta-1 antisense oligonucleotide N10.
XX
KW   Transforming growth factor beta-1; TGF beta-1; antisense oligonucleotide;
KW   modulate; gene expression; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP856579-A1.
XX
PD   05-AUG-1998.
XX
PF   31-JAN-1997;   97EP-00101531.
XX
PR   31-JAN-1997;   97EP-00101531.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Schlingensiepen K,  Brysch W;
XX
DR   WPI; 1998-400910/35.
XX
PT   Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT   consecutive guanosine or inosine - and have specific ratio of residues
PT   able to form two or three hydrogen bonds, have greater activity and
PT   reduced toxicity, used therapeutically or to modulate growth of cells in
PT   culture.
XX
PS   Example 1; Fig 3a; 286pp; English.
XX
CC   AAV48412-84 represent antisense oligonucleotides directed against
CC   transforming growth factor beta-1 (TGF beta-1). The oligonucleotides
CC   exemplify the invention. The specification describes oligonucleotides
CC   that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC   can each form three hydrogen bonds to cytosine; do not contain four
CC   consecutive nucleotides able to form three H-bonds each to four
CC   consecutive cytosines; do not contain two sequences of three consecutive
CC   nucleotides each able to form three H-bonds to three consecutive
CC   cytosines, and the ratio between residues able to form two H-bonds each
CC   (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC   oligonucleotides are used to modulate expression of genes, particularly
CC   the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC   proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC   kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC   oligonucleotides can also be used to analyse function of proteins (by
CC   altering their expression or activity) and therapeutically, e.g. in cases
CC   of cancer or (targeting TGF) for stimulating the immune system
XX
SQ   Sequence 18 BP; 1 A; 8 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
```

```
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        273 GAGCAGGGCGGCACC 287
              | || ||||||||||
Db          1 GGGCCGGGCGGCACC 15


RESULT 1137
AAZ17952
ID   AAZ17952 standard; DNA; 18 BP.
XX
AC   AAZ17952;
XX
DT   11-OCT-1999  (first entry)
XX
DE   HOX gene specific RT-PCR primer.
XX
KW   Genetic proximity; gene expression; cell characterisation; homeobox gene;
KW   genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;
KW   kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9934016-A2.
XX
PD   08-JUL-1999.
XX
PF   28-DEC-1998;   98WO-IL000625.
XX
PR   29-DEC-1997;   97IL-00122793.
PR   16-OCT-1998;   98IL-00126627.
XX
PA   (GENE-) GENENA LTD.
XX
PI   Vider B;
XX
DR   WPI; 1999-419113/35.
XX
PT   Identifying and characterizing cells by comparing the pattern of gene
PT   expression in a selected gene family.
XX
PS   Claim 4; Page 33; 102pp; English.
XX
CC   The invention provides a new method for identifying and characterising
CC   cells. The method for determining the genetic proximity of a first cell
CC   and a second cell comprises: (a) obtaining the first cell and the second
CC   cell; (b) determining in the first cell and the second cell the pattern
CC   of expression of genes in a selected gene family; and (c) calculating a
CC   proximity index using a specified formula. The methods can be used for
CC   characterising cells, e.g. for determining the origin of a cell, its
CC   genetic status, whether it carries a genetic defect, or whether it is
CC   transformed. They can be used for detecting a selected genetic defect in
CC   an individual, e.g. a fetus. They can also be used for determining the
CC   effect of a selected treatment on a test cell. They can also be used for
CC   obtaining cells capable of expressing an homeobox related desired
CC   property. The method uses reverse transcriptase polymerase chain reaction
CC   (RT-PCR) for determining the pattern of gene expression in a selected
CC   gene family. Sequences AAZ17803-Z18342 represent primers that can be used
CC   in the RT-PCR reactions to determine the pattern of gene expression. The
CC   gene family can be selected from a set of homeobox genes, kinase genes,
CC   protein phosphatase genes, P450 enzyme genes, steroid receptor
CC   superfamily genes or cadherin superfamily genes
XX
SQ   Sequence 18 BP; 5 A; 4 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         82 GCGCAGTGGACATCA 96
              ||||||||||| ||
Db          3 GCGCAGTGGACGGCA 17


RESULT 1138
AAZ28809/c
ID   AAZ28809 standard; DNA; 18 BP.
XX
AC   AAZ28809;
XX
DT   01-FEB-2000  (first entry)
XX
DE   Primer CH for MAb Fab13B5 heavy chain gene PCR amplification.
XX
KW   Peptide ligand; affinity; p24; human immune deficiency virus-1; HIV-1;
KW   light chain; heavy chain; Fab; monoclonal antibody; hypervariable region;
KW   infection; primer; PCR; amplification; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   FR2777285-A1.
XX
PD   15-OCT-1999.
XX
PF   10-APR-1998;   98FR-00004876.
XX
PR   10-APR-1998;   98FR-00004876.
XX
PA   (INMR ) BIO MERIEUX.
XX
PI   Novelli RA,  Monaco S,  Piga N,  Berthet C,  Mallet F,  Cusack S;
PI   Chassaing V;
XX
DR   WPI; 1999-593428/51.
XX
PT   New peptide ligand specific for p24 of human immune deficiency virus
PT   contains hypervariable regions of antibody 13B5, used for diagnosing HIV
PT   infection.
XX
PS   Example 1; Page 12; 27pp; French.
XX
CC   The invention relates to a peptide ligand with specific affinity for the
CC   p24 protein of human immune deficiency virus-1 (HIV-1) comprising at
CC   least one peptide strand corresponding to the N-terminal region of the
CC   light and/or heavy chain of the Fab fragment of monoclonal antibody 13B5
CC   in which: (i) the light chain includes three hypervariable regions (HVR)
CC   at amino acid (aa) positions 24-33, 49-55 and 88-95 of AAY44175; and (ii)
CC   the heavy chain includes three HVR at aa positions 26-35, 49-65 and 99-
CC   109 of AAY44176. The primers AAZ28808-Z28809 were used to PCR amplify the
CC   coding sequence for the heavy chain of Fab 13B5 (AAZ28805). The peptide
CC   ligands are reagents for detecting p24 (by standard immunoassays) in
CC   biological samples, specifically for diagnosis of HIV-1 infection or can
CC   be used to treat HIV-1 infections
XX
SQ   Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        280 GCGGCACCAAGCTGG 294
              || |||||||| |||
Db         17 GCAGCACCAAGGTGG 3


RESULT 1139
AAZ40893/c
ID   AAZ40893 standard; DNA; 18 BP.
XX
AC   AAZ40893;
XX
DT   26-JAN-2000  (first entry)
XX
```

```
DE   Human CD40 phosphorothioate antisense oligonucleotide SEQ ID NO:42.
XX
KW   Identification; genetic target; gene modulation; human; probe;
KW   antisense oligonucleotide; phosphorothioate; PCR primer;
KW   nucleotide sequence-based technology; antisense drug discovery;
KW   target validation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9953101-A1.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;   99WO-US008268.
XX
PR   13-APR-1998;   98US-0081483P.
PR   28-APR-1998;   98US-00067638.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Baker BF,  Mcneil J,  Freier SM,  Sasmor HM,  Brooks DG;
PI   Ohasi C,  Wyatt JR,  Borchers AH,  Vickers TA;
XX
DR   WPI; 1999-620446/53.
XX
PT   Identifying compounds which modulate expression of nucleic acids, used to
PT   provide compounds having defined physical, chemical or bioactive
PT   properties, e.g. antisense activity.
XX
PS   Example 8; Page 77; 264pp; English.
XX
CC   A method has been developed of defining a set of compounds that modulate
CC   the expression of a target nucleic acid (tNA) sequence via binding of the
CC   compounds with the tNA sequence. The method comprises generating a
CC   library of virtual compounds in silico according to defined criteria, and
CC   evaluating in silico the binding of the virtual compounds with the tNA
CC   according to defined criteria. Also described are: (1) a method of
CC   defining a set of oligonucleotides (ONs) that modulate the expression of
CC   a tNA sequence via binding of the ONs with the tNA sequence comprising
CC   generating a library of virtual compounds in silico according to defined
CC   criteria, and evaluating in silico the binding of the virtual ONs with
CC   the tNA according to defined criteria; and (2) a method of defining a set
CC   of compounds that modulate the expression of a tNA sequence via binding
CC   of the compounds with the tNA. The methods can be used for the generation
CC   and identification of synthetic compounds having defined physical,
CC   chemical or bioactive properties. Information gathered from assays of
CC   such compounds is used to identify nucleic acid sequences that are
CC   tractable to a variety of nucleotide sequence-based technologies, e.g.
CC   antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
CC   AAY52701 to AAY52706, represent sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 18 BP; 5 A; 4 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        128 CATGCTGGCCCGCCT 142
              ||||||  |||||  ||
Db         16 CATGCTCGCCCGGCT 2


RESULT 1140
AAV73492
ID   AAV73492 standard; DNA; 18 BP.
XX
AC   AAV73492;
XX
DT   23-FEB-1999  (first entry)
XX
DE   Human myeloid antigen-CD33 analogue GEN560D06 PCR primer F7.
XX
KW   Myeloid antigen; CD33; detection; gene expression; analogue; GEN 560D06;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   JP10286089-A.
XX
PD   27-OCT-1998.
XX
PF   15-APR-1997;   97JP-00096908.
XX
PR   15-APR-1997;   97JP-00096908.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 1999-063481/06.
XX
PT   New human rab7GTP-combined analogous protein gene - useful for detection
PT   of its expression in tissues.
XX
PS   Example 2; Page 10; 35pp; Japanese.
XX
CC   AAV73492 and AAV73493 are PCR primers used in the amplification of a
CC   novel human myeloid antigen-CD33 connecting protein analogue, GEN 560D06.
CC   The gene is useful for the detection of gene expression in various
CC   tissues
XX
SQ   Sequence 18 BP; 1 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        241 GCTGCTTCCCGGGCT 255
              ||||  ||||  |||||
Db          1 GCTGGTTCCAGGGCT 15


RESULT 1141
AAX38029
ID   AAX38029 standard; DNA; 18 BP.
XX
AC   AAX38029;
XX
DT   04-JUN-1999  (first entry)
XX
DE   HLA-A untranslated region primer SEQ ID NO:185.
XX
KW   Human; histocompatibility locus antigen; HLA; determination; allele;
KW   HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9907883-A1.
XX
PD   18-FEB-1999.
XX
PF   11-AUG-1998;   98WO-CA000768.
XX
PR   11-AUG-1997;   97US-00909290.
XX
PA   (VISI-) VISIBLE GENETICS INC.
PA   (BLAS/) BLASCZYK R H.
XX
PI   Blasczyk RH,  Leushner J;
XX
DR   WPI; 1999-167446/14.
XX
PT   Determination of HLA class I group type of a subject - using group
PT   specific untranslated region primer pair.
```

```
XX
PS   Disclosure; Page 18; 195pp; English.
XX
CC   The present invention describes a method using novel primers involving
CC   the PCR-based determination of histocompatibility locus antigen B (HLA-B)
CC   Class I group type. Determining the HLA-B Class I group type of a subject
CC   comprises: (i) combining a group-specific untranslated region primer pair
CC   with a target DNA sample from the subject under conditions such that
CC   primer-based amplification of the target DNA may occur; and (ii)
CC   determining whether a nucleic acid product is produced by the
CC   amplification; where the ability of the primer pair to produce a nucleic
CC   acid product is associated with a particular HLA group type. The method
CC   can be used for HLA-B typing. In the method, the initial group specific
CC   amplification allows a PCR based separation of haplotypes in 95% of
CC   patient samples. It permits the resolution of cis/trans linkages of
CC   heterozygote sequencing results which cannot be achieved with other
CC   protocols. AAX37845 to AAX38286 represent DNA sequence used in the
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 2 A; 5 C; 10 G; 1 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        138 CGCCTGGCGGTGGAG 152
              ||||||||||  || |
Db          1 CGCCTGGCGGGGGGG 15


RESULT 1142
AAX38246
ID   AAX38246 standard; DNA; 18 BP.
XX
AC   AAX38246;
XX
DT   04-JUN-1999  (first entry)
XX
DE   Histocompatibility locus antigen PCR primer SEQ ID NO:402.
XX
KW   Human; histocompatibility locus antigen; HLA; determination; allele;
KW   HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9907883-A1.
XX
PD   18-FEB-1999.
XX
PF   11-AUG-1998;   98WO-CA000768.
XX
PR   11-AUG-1997;   97US-00909290.
XX
PA   (VISI-) VISIBLE GENETICS INC.
PA   (BLAS/) BLASCZYK R H.
XX
PI   Blasczyk RH,  Leushner J;
XX
DR   WPI; 1999-167446/14.
XX
PT   Determination of HLA class I group type of a subject - using group
PT   specific untranslated region primer pair.
XX
PS   Example; Page 28; 195pp; English.
XX
CC   The present invention describes a method using novel primers involving
CC   the PCR-based determination of histocompatibility locus antigen B (HLA-B)
CC   Class I group type. Determining the HLA-B Class I group type of a subject
CC   comprises: (i) combining a group-specific untranslated region primer pair
CC   with a target DNA sample from the subject under conditions such that
CC   primer-based amplification of the target DNA may occur; and (ii)
CC   determining whether a nucleic acid product is produced by the
CC   amplification; where the ability of the primer pair to produce a nucleic
CC   acid product is associated with a particular HLA group type. The method
CC   can be used for HLA-B typing. In the method, the initial group specific
CC   amplification allows a PCR based separation of haplotypes in 95% of
CC   patient samples. It permits the resolution of cis/trans linkages of
CC   heterozygote sequencing results which cannot be achieved with other
CC   protocols. AAX37845 to AAX38286 represent DNA sequence used in the
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 TGACCGAGGGCTGGG 36
              ||||||||  |||||
Db          2 TGACCGAGACCTGGG 16


RESULT 1143
AAZ30566
ID   AAZ30566 standard; DNA; 18 BP.
XX
AC   AAZ30566;
XX
DT   18-JAN-2000  (first entry)
XX
DE   Human integrin alpha 4 gene antisense oligonucleotide ISIS #24449.
XX
KW   Human; integrin; antisense; oligonucleotide; inhibition; expression;
KW   very late antigen; CD49d; CD29; cell surface; leucocyte; adhesion;
KW   vascular endothelial cell; vascular endothelium; migration; inflammation;
KW   atherosclerosis; allergy; asthma; rheumatoid arthritis; tumor;
KW   metastasis; circulatory system; autoimmune disease; Grave's disease;
KW   Hashimoto's thyroiditis; encephalomyelitis; multiple sclerosis; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5968826-A.
XX
PD   19-OCT-1999.
XX
PF   05-OCT-1998;   98US-00166203.
XX
PR   05-OCT-1998;   98US-00166203.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Cowsert LM,  Condon TP;
XX
DR   WPI; 1999-590416/50.
XX
PT   Antisense inhibition of integrin alpha4 expression useful for treating
PT   inflammatory diseases such as atherosclerosis, allergies, asthma and
PT   arthritis.
XX
PS   Example 8; Col 25; 40pp; English.
XX
CC   The invention relates to the generation of antisense oligonucleotides
CC   targeted to the integrin alpha4 gene (human sequence AAZ30555) which are
CC   used for inhibiting expression of the integrin alpha4 mRNA or protein.
CC   The oligonucleotides AAZ30556-Z30594 are used to inhibit human integrin
CC   alpha4 protein expression. Integrin alpha4 is a component of Very Late
CC   Antigen (VLA)-4 (also called alpha4beta1 and CD49d/CD29). VLA-4 is
CC   expressed on the cell surfaces of leucocytes and vascular endothelial
CC   cells and mediates the adhesion of leucocytes to the vascular endothelium
CC   prior to migration into the surrounding tissues. This migration is an
CC   essential step in inflammation and hence VLA-4 (and consequently integrin
CC   alpha4) is a potential therapeutic target for treating inflammatory
CC   diseases and the damaging effects of excessive inflammation. These
CC   disorders include atherosclerosis, allergies, asthma, rheumatoid
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CC   arthritis and tumor cell metastasis (VLA-4 is involved in migration of
CC   the tumor cells through the extracellular matrix into the circulatory
CC   system). VLA-4 is also involved in a number of autoimmune diseases such
CC   as Grave's disease, Hashimoto's thyroiditis, encephalomyelitis (EAE),
CC   multiple sclerosis. VLA-4 may also be involved in promoting adhesion
CC   (i.e. retention) of hemopoietic stem cells in bone-marrow and in
CC   allograft rejection
XX
SQ   Sequence 18 BP; 2 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         98 CACGTCTGACCGCGA 112
              ||||||| ||| ||
Db          2 CACGTCTGGCCGGGA 16


RESULT 1144
AAA57864
ID   AAA57864 standard; DNA; 18 BP.
XX
AC   AAA57864;
XX
DT   11-OCT-2000  (first entry)
XX
DE   Mutant effector oligonucleotide, mut.3.
XX
KW   Ribozyme; catalytic RNA; analyte detection; effector molecule;
KW   nucleic acid substrate; in vitro selection; ribozyme ligase;
KW   conformation dependent activity; allosteric activation; mutant; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .18
FT                   /*tag=  a
FT                   /bound_moiety= "Bases 120-136 of ribosome ligase L1
FT                   (AAA57859)"
XX
PN   WO200024931-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-IL000557.
XX
PR   23-OCT-1998;   98IL-00126731.
XX
PA   (INTE-) INTELLIGENE LTD.
XX
PI   Nathan A,  Ellington A;
XX
DR   WPI; 2000-350763/30.
XX
PT   Detecting an analyte in a sample comprises providing nucleic acid
PT   sequence which is catalytically active in presence of analyte, contacting
PT   catalytic nucleic acid with substrate and amplifying catalytic product.
XX
PS   Example 3; Page 17; 36pp; English.
XX
CC   The invention relates to a method of detecting an analyte in a sample.
CC   The method comprises providing a nucleic acid sequence which is initially
CC   catalytically inactive, but which becomes catalytically active in the
CC   presence of an analyte (the effector); providing a nucleic acid substrate
CC   for the catalytic activity of the nucleic acid sequence; and contacting
CC   the nucleic acid sequence and the substrate with the sample under
CC   conditions allowing catalytic activity of nucleic acid sequences. The
CC   catalytic nucleic acid sequence will be able to convert the nucleic acid
CC   substrate into a nucleic acid product only if the analyte of interest is
CC   present. The nucleic acid catalytic product is then amplified, and a
CC   significant increase in the amount of product indicates the presence of
CC   the analyte in the sample. The method is useful for the qualitative or
CC   quantitative determination of an analyte in a sample in diagnostic
CC   assays. The invention describes the in vitro selection of a ribozyme
CC   ligase (L1; AAA57859, AAA57860) which is catalytically active only in the
CC   presence of an oligonucleotide effector (AAA57854). The L1 ribozyme
CC   ligase was selected from a pool of RNA molecules comprising a central
CC   randomised region 90 nucleotides in length flanked on both sides by
CC   constant sequence regions (the N90 RNA pool; AAA57851). In the presence
CC   of the effector, selection was performed using one of the tagged
CC   substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,
CC   those which have become ligated to the substrate molecule) were reverse
CC   transcribed using the effector oligo, and then PCR amplified using the
CC   effector and a DNA primer identical in sequence to the substrate used for
CC   the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC   can only adopt its active conformation (AAA57859) in the presence of the
CC   effector oligo (analyte). In the absence of the effector, L1 adopts an
CC   inactive conformation (AAA57860). Sequences AAA57863-A57867 represent a
CC   series of mutant effector oligonucleotide used with wild-type L1 ribozyme
CC   (AAA57859) in an exemplification of the invention
XX
SQ   Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         86 AGTGGACATCACCAC 100
              | |||||||||| ||
Db          4 ACTGGACATCACGAC 18


RESULT 1145
AAZ47726/c
ID   AAZ47726 standard; DNA; 18 BP.
XX
AC   AAZ47726;
XX
DT   02-MAR-2000  (first entry)
XX
DE   Human CD40 antisense oligonucleotide SEQ ID NO:42.
XX
KW   Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
KW   expression; immune disease; inflammatory disease; immunomodulatory;
KW   anti-inflammatory; anti-arthritic; anti-asthmatic; antiproliferative;
KW   anticancer; immuno-suppressive; anti-psoriaritic; allograft rejection;
KW   hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
KW   inflammatory bowel disease; asthma; psoriasis; cancer; tumour; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9957320-A1.
XX
PD   11-NOV-1999.
XX
PF   22-APR-1999;   99WO-US008765.
XX
PR   01-MAY-1998;   98US-00071433.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Cowsert LM;
XX
DR   WPI; 2000-062158/05.
XX
PT   Antisense molecules directed against nucleic acid encoding human CD40,
PT   for treating e.g. immune, inflammatory or hyperproliferative diseases.
XX
PS   Example 9; Page 44; 102pp; English.
XX
CC   AAZ47685 to AAZ47768 represent phosphorothioate antisense
CC   oligonucleotides targeted to human CD40, which can be used to inhibit the
CC   expression of human CD40. CD40 is involved in lymphocyte activation,
CC   tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
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CC   prevent immune-associated diseases (specifically guest vs. host disease,
CC   allograft rejection or autoimmune diseases); inflammation (specifically
CC   asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
CC   disease or psoriasis) or hyperproliferation (specifically cancer and
CC   tumours). the antisense oligonucleotides are also useful as diagnostic
CC   and research reagents. AAZ47769 represents the human CD40 nucleotide
CC   sequence. AAZ47770 to AAZ47772 represent human CD40 forward and reverse
CC   PCR primers, and a human CD40 PCR probe, respectively. AAZ47773 to
CC   AAZ47775 represent other PCR primers and a probe used in the
CC   exemplification of the present invention
XX
SQ   Sequence 18 BP; 5 A; 4 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        128 CATGCTGGCCCGCCT 142
              ||||||  |||||  ||
Db         16 CATGCTCGCCCGGCT 2


RESULT 1146
AAZ98706/c
ID   AAZ98706 standard; DNA; 18 BP.
XX
AC   AAZ98706;
XX
DT   20-JUN-2000  (first entry)
XX
DE   Collagen promoter inhibitory oligonucleotide Oligo 147 P.
XX
KW   Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
KW   atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
KW   peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
XX
OS   Rattus sp.
XX
PN   WO200008213-A1.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US017824.
XX
PR   07-AUG-1998;   98US-00130888.
XX
PA   (GUNT/) GUNTAKA R V.
XX
PI   Guntaka RV,  Weber KT,  Kovacs A,  Kandala J;
XX
DR   WPI; 2000-205739/18.
XX
PT   Inhibitors of collagen gene useful for treating fibrosis associated with
PT   atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
PT   comprises oligomers capable of inhibiting collagen gene.
XX
PS   Claim 19; Fig 8; 77pp; English.
XX
CC   This sequence represents an oligomer which is capable of inhibiting the
CC   expression of the collagen gene. The oligomer is capable of binding to
CC   the promoter region of the collagen gene. Collagen is a family of fibrous
CC   proteins, and is the major element of skin, bone, tendon, cartilage,
CC   blood vessels and teeth. The oligomers are useful for inhibiting
CC   expression of the collagen gene, comprising inserting the oligomers into
CC   a cell and causing an intracellular reaction to inhibit the gene
CC   expression. The collagen inhibitory oligomers of the invention are useful
CC   for treating pathological fibrosis associated with myocardial fibrosis in
CC   hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
CC   lung fibrosis, peritoneal fibrosis and skin fibrosis found in
CC   scleroderma, hypertrophic scars and burn injury
XX
SQ   Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 CTTCCTCACTTTCCT 376
              | |||||  |||||||
Db         18 CCTCCTCCCTTTCCT 4


RESULT 1147
AAZ98715/c
ID   AAZ98715 standard; DNA; 18 BP.
XX
AC   AAZ98715;
XX
DT   20-JUN-2000  (first entry)
XX
DE   Collagen promoter inhibitory oligonucleotide Oligo Col 164 APS.
XX
KW   Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
KW   atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
KW   peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
XX
OS   Rattus sp.
XX
PN   WO200008213-A1.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US017824.
XX
PR   07-AUG-1998;   98US-00130888.
XX
PA   (GUNT/) GUNTAKA R V.
XX
PI   Guntaka RV,  Weber KT,  Kovacs A,  Kandala J;
XX
DR   WPI; 2000-205739/18.
XX
PT   Inhibitors of collagen gene useful for treating fibrosis associated with
PT   atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
PT   comprises oligomers capable of inhibiting collagen gene.
XX
PS   Example 4; Fig 8; 77pp; English.
XX
CC   This sequence represents an oligomer which is capable of inhibiting the
CC   expression of the collagen gene. The oligomer is capable of binding to
CC   the promoter region of the collagen gene. Collagen is a family of fibrous
CC   proteins, and is the major element of skin, bone, tendon, cartilage,
CC   blood vessels and teeth. The oligomers are useful for inhibiting
CC   expression of the collagen gene, comprising inserting the oligomers into
CC   a cell and causing an intracellular reaction to inhibit the gene
CC   expression. The collagen inhibitory oligomers of the invention are useful
CC   for treating pathological fibrosis associated with myocardial fibrosis in
CC   hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
CC   lung fibrosis, peritoneal fibrosis and skin fibrosis found in
CC   scleroderma, hypertrophic scars and burn injury
XX
SQ   Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 CTTCCTCACTTTCCT 376
              | |||||  |||||||
Db         18 CCTCCTCCCTTTCCT 4


RESULT 1148
AAZ98708/c
ID   AAZ98708 standard; DNA; 18 BP.
XX
```

```
AC   AAZ98708;
XX
DT   20-JUN-2000  (first entry)
XX
DE   Collagen promoter inhibitory oligonucleotide Oligo Col 164 APS.
XX
KW   Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
KW   atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
KW   peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
XX
OS   Rattus sp.
XX
PN   WO200008213-A1.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-US017824.
XX
PR   07-AUG-1998;   98US-00130888.
XX
PA   (GUNT/) GUNTAKA R V.
XX
PI   Guntaka RV,  Weber KT,  Kovacs A,  Kandala J;
XX
DR   WPI; 2000-205739/18.
XX
PT   Inhibitors of collagen gene useful for treating fibrosis associated with
PT   atherosclerosis, restenosis, liver cirrhosis, lung and skin fibrosis,
PT   comprises oligomers capable of inhibiting collagen gene.
XX
PS   Claim 19; Fig 8; 77pp; English.
XX
CC   This sequence represents an oligomer which is capable of inhibiting the
CC   expression of the collagen gene. The oligomer is capable of binding to
CC   the promoter region of the collagen gene. Collagen is a family of fibrous
CC   proteins, and is the major element of skin, bone, tendon, cartilage,
CC   blood vessels and teeth. The oligomers are useful for inhibiting
CC   expression of the collagen gene, comprising inserting the oligomers into
CC   a cell and causing an intracellular reaction to inhibit the gene
CC   expression. The collagen inhibitory oligomers of the invention are useful
CC   for treating pathological fibrosis associated with myocardial fibrosis in
CC   hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
CC   lung fibrosis, peritoneal fibrosis and skin fibrosis found in
CC   scleroderma, hypertrophic scars and burn injury
XX
SQ   Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 CTTCCTCACTTTCCT 376
              | ||||| |||||||
Db         18 CCTCCTCCCTTTCCT 4


RESULT 1149
AAZ57673/c
ID   AAZ57673 standard; DNA; 18 BP.
XX
AC   AAZ57673;
XX
DT   05-APR-2000  (first entry)
XX
DE   Human G-alpha-12 antisense inhibitor ISIS# 20661.
XX
KW   G-alpha-12 inhibitor; antisense compound; cell differentiation; cancer;
KW   cell growth; metastatic growth; ss; ISIS# 20661.
XX
OS   Homo sapiens.
XX
PN   US5998206-A.
XX
PD   07-DEC-1999.
XX
PF   23-FEB-1999;   99US-00256496.
XX
PR   23-FEB-1999;   99US-00256496.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-095920/08.
XX
PT   Antisense inhibition of human G-alpha-12 expression.
XX
PS   Example 15; Col 38; 36pp; English.
XX
CC   This is a human G-alpha-12 antisense nucleotide sequence. G-alpha-12 is a
CC   member of the G12/13 subfamily of G-proteins. The primary function of G-
CC   alpha-12 is in cell differentiation and growth. The invention relates to
CC   antisense compounds which are 8-30 nucleotides long (see AAZ57668-
CC   Z57746). The antisense molecules are targeted to the human G-alpha-12
CC   nucleic acid molecule, and inhibit the expression of G-alpha-12. The
CC   molecules preferably have a modified internucleotide linkage, and at
CC   least one modified sugar moiety. The compounds target different regions
CC   of the human G-alpha-12 RNA. The expression of human G-alpha 12 is
CC   inhibited by contacting human cells or tissues in vitro with the
CC   antisense molecules. The oligonucleotides are used in modulating the
CC   function of nucleic acid molecules encoding G-alpha-12, ultimately
CC   modulating the amount of G-alpha-12 produced. The antisense compounds can
CC   be utilized for diagnostics, therapeutics, prophylaxis and as research
CC   agents and kits. They may be useful in the treatment of cancer, and
CC   metastatic growth
XX
SQ   Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 CTGGTGAAGGACCTG 305
              |||||||||  ||||
Db         16 CTGGTGAAGATCCTG 2


RESULT 1150
AAZ91392/c
ID   AAZ91392 standard; DNA; 18 BP.
XX
AC   AAZ91392;
XX
DT   22-MAY-2000  (first entry)
XX
DE   Human PTEN phosphorothioate antisense oligonucleotide #29558.
XX
KW   Human; PTEN; MMAC1; TEP1; phosphorothioate; antisense oligonucleotide;
KW   inhibition; protein phosphatase; tumour; diagnosis; inflammation;
KW   anticancer; anti-inflammatory; anti-infective; infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /note= "phosphorothioate linkages"
XX
PN   US6020199-A.
XX
PD   01-FEB-2000.
XX
PF   21-JUL-1999;   99US-00358381.
XX
PR   21-JUL-1999;   99US-00358381.
XX
```

```
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-181363/16.
XX
PT   New antisense compounds useful for treating, preventing or diagnosing
PT   e.g. tumors or inflammation, are targeted to the human dual specificity
PT   protein phosphatase (PTEN) sequence.
XX
PS   Example 15; Col 41; 32pp; English.
XX
CC   The present invention describes phosphorothioate antisense
CC   oligonucleotides that are targeted to the 3'-untranslated region (UTR) of
CC   the sequence encoding a human dual specificity protein phosphatase
CC   designated PTEN (also known as MMAC1 and TEP1), and hybridise
CC   specifically to the human PTEN nucleotide sequence given in AAZ91361. The
CC   antisense oligonucleotides have anticancer, anti-inflammatory and anti-
CC   infective activities. The phosphorothioate antisense oligonucleotides can
CC   be used for diagnosis, treatment and prevention of PTEN-related diseases,
CC   e.g. infections, inflammation and tumours. The present sequence
CC   represents a phosphorothioate antisense oligonucleotide for human PTEN,
CC   from the present invention
XX
SQ   Sequence 18 BP; 6 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        406 TCTACGTGATCGAGA 420
              |||| |||||| |||
Db         18 TCTATGTGATCAAGA 4


RESULT 1151
AAZ93459
ID   AAZ93459 standard; DNA; 18 BP.
XX
AC   AAZ93459;
XX
DT   24-JUL-2000  (first entry)
XX
DE   TRADD antisense oligonucleotide.
XX
KW   TRADD; TNF; tumour necrosis factor; NF-kappa-B; apoptosis;
KW   programmed cell death; antisense; inhibition; treatment; therapy;
KW   septic shock; inflammation; cancer; antiinflammatory; human; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    complement(1. .18)
FT                   /*tag=  a
FT                   /note= "Complementary to bases 389-372 of the human TRADD
FT                   sequence described in GENESEQ record AAZ93431"
XX
PN   WO200012527-A1.
XX
PD   09-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019614.
XX
PR   28-AUG-1998;   98US-00143212.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-237846/20.
XX
PT   New antisense compounds that limit the expression of human TRADD protein,
PT   useful in the treatment and diagnosis of cancer, inflammation and septic
PT   shock.
XX
PS   Claim 3; Page 51; 85pp; English.
XX
CC   The intracellular protein TRADD has been identified as a critical link
CC   between tumour necrosis factor (TNF) receptor binding and downstream
CC   activation of NF-kappa-B. Overexpression of native TRADD activates NF-
CC   kappa-B in the absence of TNF and dominant negative mutants of TRADD
CC   block TNF-induced NF-kappa-B activation. A second effect of TNF in many
CC   cell types is the induction of apoptosis (programmed cell death). TRADD
CC   overexpression has been shown to mimic TNF induction of apoptosis as
CC   well. Data indicates that TRADD and other downstream effector proteins
CC   are the rate limiting step of TNF action and would therefore serve as the
CC   most efficient targets for inhibition of TNF-induced events. Antisense
CC   oligonucleotides capable of inhibiting TRADD function may therefore be
CC   useful in a number of therapeutic, diagnostic and research applications.
CC   Inhibiting expression of TRADD by contacting human cells or tissues with
CC   the antisense compound may be used to treat a disease or condition
CC   associated with TRADD expression, for example, septic shock,
CC   inflammation, or cancer. TRADD antisense oligonucleotides of varying
CC   inhibitory capabilities are listed in GENESEQ records AAZ93438-Z93517.
CC   The antisense oligonucleotides exhibit enhanced inhibitory capabilities
CC   when they have 2'-MOE wings and a deoxy gap
XX
SQ   Sequence 18 BP; 3 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        313 GGGACCGCGTGCTGG 327
              || |||| |||||||
Db          4 GGCACCGAGTGCTGG 18


RESULT 1152
AAZ93461/c
ID   AAZ93461 standard; DNA; 18 BP.
XX
AC   AAZ93461;
XX
DT   24-JUL-2000  (first entry)
XX
DE   TRADD antisense oligonucleotide.
XX
KW   TRADD; TNF; tumour necrosis factor; NF-kappa-B; apoptosis;
KW   programmed cell death; antisense; inhibition; treatment; therapy;
KW   septic shock; inflammation; cancer; antiinflammatory; human; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    complement(1. .18)
FT                   /*tag=  a
FT                   /note= "Complementary to bases 401-384 of the human TRADD
FT                   sequence described in GENESEQ record AAZ93431"
XX
PN   WO200012527-A1.
XX
PD   09-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019614.
XX
PR   28-AUG-1998;   98US-00143212.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-237846/20.
XX
PT   New antisense compounds that limit the expression of human TRADD protein,
PT   useful in the treatment and diagnosis of cancer, inflammation and septic
```

PT shock.
XX
PS Claim 3; Page 52; 85pp; English.
XX
CC The intracellular protein TRADD has been identified as a critical link
CC between tumour necrosis factor (TNF) receptor binding and downstream
CC activation of NF-kappa-B. Overexpression of native TRADD activates NF-
CC kappa-B in the absence of TNF and dominant negative mutants of TRADD
CC block TNF-induced NF-kappa-B activation. A second effect of TNF in many
CC cell types is the induction of apoptosis (programmed cell death). TRADD
CC overexpression has been shown to mimic TNF induction of apoptosis as
CC well. Data indicates that TRADD and other downstream effector proteins
CC are the rate limiting step of TNF action and would therefore serve as the
CC most efficient targets for inhibition of TNF-induced events. Antisense
CC oligonucleotides capable of inhibiting TRADD function may therefore be
CC useful in a number of therapeutic, diagnostic and research applications.
CC Inhibiting expression of TRADD by contacting human cells or tissues with
CC the antisense compound may be used to treat a disease or condition
CC associated with TRADD expression, for example, septic shock,
CC inflammation, or cancer. TRADD antisense oligonucleotides of varying
CC inhibitory capabilities are listed in GENESEQ records AAZ93438-Z93517.
CC The antisense oligonucleotides exhibit enhanced inhibitory capabilities
CC when they have 2'-MOE wings and a deoxy gap
XX
SQ Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 262 CGGTGCACCTGGAGC 276
|| |||| |||||||
Db 16 CGCTGCAACTGGAGC 2

RESULT 1153
AAC70705
ID AAC70705 standard; DNA; 18 BP.
XX
AC AAC70705;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism PCR primer #357.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
PS Claim 8; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 236 GGGAGGCTGCTTCCC 250
| |||||| ||||||
Db 1 GAGAGGCTCCTTCCC 15

RESULT 1154
AAA52014
ID AAA52014 standard; cDNA; 18 BP.
XX
AC AAA52014;
XX
DT 19-DEC-2000 (first entry)
XX
DE Antisense oligonucleotide directed against PI3K p85 subunit.
XX
KW Phosphatidylinositol 3-kinase; PI3K; p85; p110; heterodimer; hormone;
KW growth factor; receptor; antisense; inhibition; expression; diagnosis;
KW modulation; growth factor mediated cell transformation; mitogenesis;
KW protein trafficking; cell survival; cell proliferation; DNA synthesis;
KW apoptosis; neurite outgrowth; insulin-stimulated glucose transport; ss.
XX
OS Synthetic.
XX
PN US6100090-A.
XX
PD 08-AUG-2000.
XX
PF 25-JUN-1999; 99US-00344521.
XX
PR 25-JUN-1999; 99US-00344521.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM;
XX
DR WPI; 2000-542426/49.
XX
PT Antisense compounds targeted to the coding region of human
PT phosphatidylinositol 3-kinase (pI3K) p85 and inhibiting pI3K p85
PT expression, useful for treating disorders associated with pI3K p85
PT expression.
XX
PS Claim 11; Col 39; 32pp; English.
XX
CC The phosphatidylinositol 3-kinases (PI3Ks) represent a ubiquitous family
CC of heterodimeric lipid kinases that are found in association with the
CC cytoplasmic domain of hormone and growth factor receptors and oncogene
CC products. PI3Ks act as downstream effectors of these receptors, are
CC recruited upon receptor stimulation and mediate the activation of second
CC messenger signaling pathways. The PI3 kinase enzyme consists of a 110kD
CC catalytic subunit (p110) associated with an 85kD regulatory subunit (p85)
CC and it is through the SH2 domains of the p85 subunit that the enzyme
CC associates with the membrane bound receptors. PI3Ks have been implicated
CC in many cellular activities including growth factor mediated cell
CC transformation, mitogenesis, protein trafficking, cell survival and
CC proliferation, DNA synthesis, apoptosis, neurite outgrowth and insulin-

```
CC   stimulated glucose transport. Antisense compounds directed against PI3K
CC   p85 and which inhibit its expression are useful as diagnostics and
CC   research reagents, and as a component of kits, which can be used for
CC   detecting the level of pI3K p85 in a sample. The compounds may be
CC   administered to an animal or human suspected of having a disease or
CC   disorder which can be treated by modulating the expression of PI3K p85.
CC   The compounds may further be useful prophylactically, e.g., to prevent or
CC   delay infection, inflammation or tumour formation. The target site of
CC   this antisense molecule is nucleotide 88 of the coding region of the PI3K
CC   p85 subunit (See GENESEQ record AAA52007)
XX
SQ   Sequence 18 BP; 1 A; 6 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 CTTCCTCACTTTCCT 376
              |||| || |||||||
Db          3 CTTCTTCTCTTTCCT 17


RESULT 1155
AAA63428/c
ID   AAA63428 standard; DNA; 18 BP.
XX
AC   AAA63428;
XX
DT   06-MAR-2001  (first entry)
XX
DE   C-1027 gene cluster reverse PCR primer for ORF 30.
XX
KW   Enediyne C-1027 biosynthesis gene cluster; apoprotein; chromophore;
KW   PCR primer; ss.
XX
OS   Streptomyces globisporus.
XX
PN   WO200040596-A1.
XX
PD   13-JUL-2000.
XX
PF   06-JAN-2000; 2000WO-US000446.
XX
PR   06-JAN-1999;   99US-0115434P.
PR   05-JAN-2000; 2000US-00477962.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Shen B,  Liu W,  Christenson SD,  Standage S;
XX
DR   WPI; 2000-465947/40.
XX
PT   Isolated nucleic acid comprising a nucleic acid encoding any of C-1027
PT   open reading frames (ORFs) -7 to 42, excluding ORF 9 (cagA), useful for
PT   the production of enediyne C-1027 antitumor antibiotics.
XX
PS   Disclosure; Page 18; 160pp; English.
XX
CC   The present invention is concerned with the elucidation of the gene
CC   cluster from Streptomyces globisporus which regulates enediyne C-1027
CC   synthesis. Enediyne C-1027 is an antibiotic, consisting of an apoprotein
CC   and a non-peptidic chromophore, which causes damage to DNA. The primers
CC   AAA63353-A63451 were used to isolate the open reading frames which
CC   comprise the gene cluster. The sequences within the gene cluster can be
CC   used to produce the protein and to identify antagonists, both of which
CC   can be used in the treatment of cancer
XX
SQ   Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        260 CACGGTGCACCTGGA 274
              |||| |||||||| |
Db         18 CACGCTGCACCTGCA 4


RESULT 1156
AAA95335/c
ID   AAA95335 standard; DNA; 18 BP.
XX
AC   AAA95335;
XX
DT   12-FEB-2001  (first entry)
XX
DE   B. cereus zwittermicin A coding sequence sequencing primer #19.
XX
KW   Zwittermicin A; aminopolyol antibiotic; crop protection; phytopathogen;
KW   biocontrol agent; infectious disease; PCR primer; ss.
XX
OS   Bacillus cereus.
XX
PN   WO200058351-A2.
XX
PD   05-OCT-2000.
XX
PF   22-MAR-2000; 2000WO-US007570.
XX
PR   23-MAR-1999;   99US-0125769P.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Handelsman J,  Milner JL,  Stohl EA,  Emmert EA;
XX
DR   WPI; 2000-647222/62.
XX
PT   Novel Bacillus cereus nucleic acid molecule useful for synthesis of
PT   zwittermicin A for protecting crops against phytopathogens.
XX
PS   Example 1; Page 22; 80pp; English.
XX
CC   The present invention describes the coding sequence for the enzymes from
CC   Bacillus cereus which form the zwittermicin A aminopolyol antibiotic.
CC   These enzymes are known as Orf1, Orf2, Orf3 and ZmaR. The antibiotic is
CC   useful in plants as a biocontrol agent as it help protect them from
CC   phytopathogens, which destroy crops. In addition, the coding sequence and
CC   proteins are useful for the treatment of human infectious diseases. The
CC   present sequence is a primer used to sequence the zwittermicin A genes
XX
SQ   Sequence 18 BP; 8 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        193 TCCACTGCTCGGTGA 207
              |||||| |||| |||
Db         17 TCCACTTCTCGTTGA 3


RESULT 1157
AAF62691/c
ID   AAF62691 standard; DNA; 18 BP.
XX
AC   AAF62691;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Primer kcs 3.
XX
KW   Long chain fatty acid condensing enzyme; KCS2;
KW   beta-ketoacyl-coenzyme A synthase 2; cosuppression; antisense; screening;
KW   ss.
XX
OS   Arabidopsis sp.
```

```
XX
PN   WO200107586-A2.
XX
PD   01-FEB-2001.
XX
PF   21-JUL-2000; 2000WO-CA000860.
XX
PR   22-JUL-1999;   99US-0145013P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Kunst L,  Clemens S;
XX
DR   WPI; 2001-168548/17.
XX
PT   Novel nucleic acid sequence encoding plant long chain fatty acid (LCFA)
PT   condensing enzyme (fatty acid elongase) useful for producing transgenic
PT   plants having altered fatty acid content in the tissues.
XX
PS   Example 1; Page 16; 32pp; English.
XX
CC   The present invention relates to a plant long chain fatty acid condensing
CC   enzyme, KCS2 (beta-ketoacyl-coenzyme A synthase 2). The invention is
CC   useful in cosuppression or antisense inhibition, as a plant breeding
CC   tool, as molecular markers to aid in plant breeding programs and in
CC   screening
XX
SQ   Sequence 18 BP; 7 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        403 TCTTCTACGTGATCG 417
              ||| || ||||||||
Db         15 TCTACTCCGTGATCG 1


RESULT 1158
AAF79669/c
ID   AAF79669 standard; DNA; 18 BP.
XX
AC   AAF79669;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Human Akt-3 antisense oligonucleotide, SEQ ID NO: 77.
XX
KW   Human; Akt-3; protein kinase; cytostatic; antiinflammatory; infection;
KW   antisense therapy; inflammation; tumour; ss.
XX
OS   Homo sapiens.
XX
PN   US6187586-B1.
XX
PD   13-FEB-2001.
XX
PF   29-DEC-1999;   99US-00474922.
XX
PR   29-DEC-1999;   99US-00474922.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM,  Roth RA;
XX
DR   WPI; 2001-264979/27.
XX
PT   New antisense compounds targeting nucleic acids encoding human Akt-3
PT   useful for treating a disease or condition associated with Akt-3
PT   expression, or in preventing or delaying inflammation or tumor formation.
XX
PS   Claim 1; Col 40; 37pp; English.
XX
CC   The present sequence is one of a number of antisense compounds of up to
CC   30 nucleobases in length targeted to a nucleic acid encoding human Akt-3.
CC   The antisense compounds are useful for inhibiting the expression of human
CC   Akt-3 in human cells or tissues. They are also useful for modulating the
CC   expression of Akt-3, and for treating a human or an animal suspected of
CC   having, or being prone to, a disease or condition associated with Akt-3
CC   expression. The antisense compounds may also be used as research
CC   reagents, in kits and in diagnostics, e.g. to elucidate the function of a
CC   particular gene or to distinguish between functions of various members of
CC   a biological pathway; and as a prophylactic, e.g. to prevent or delay
CC   infection, inflammation or tumour formation
XX
SQ   Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        292 TGGTGAAGGACCTGA 306
              ||||| |||||| ||
Db         15 TGGTGGAGGACCAGA 1


RESULT 1159
AAF99484/c
ID   AAF99484 standard; DNA; 18 BP.
XX
AC   AAF99484;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #600.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 51; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
```

```
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 18 BP; 0 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        379 ACCGCGACGACGGCG 393
              |||||  ||||||||
Db         15 ACCGCCGCGACGGCG 1


RESULT 1160
AAH75367/c
ID   AAH75367 standard; DNA; 18 BP.
XX
AC   AAH75367;
XX
DT   02-OCT-2001  (first entry)
XX
DE   Atrophaneura alcinous protein 3' RACE primer 3.
XX
KW   Lepidopteran; insect; agricultural chemical development; PCR primer; ss.
XX
OS   Atrophaneura alcinous.
OS   Synthetic.
XX
PN   JP2001128689-A.
XX
PD   15-MAY-2001.
XX
PF   09-AUG-2000; 2000JP-00241272.
XX
PR   24-AUG-1999;   99JP-00236700.
XX
PA   (SUNR ) SUNTORY LTD.
XX
DR   WPI; 2001-445694/48.
XX
PT   New protein derived from leidopteran insects, useful for screening of
PT   oviposition control substance.
XX
PS   Example 3; Page 6; 13pp; Japanese.
XX
CC   The invention relates to a protein derived from lepidopteran insects,
CC   especially a protein obtained from the fore-legs of Atrophaneura alcinous
CC   useful in the development of agricultural chemicals. The present sequence
CC   is that of a 3' RACE primer of the invention
XX
SQ   Sequence 18 BP; 4 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         35 GGACGAAGATGGCCA 49
              ||  |||||  ||||||
Db         18 GGTCGAAGTTGGCCA 4


RESULT 1161
AAS14018/c
ID   AAS14018 standard; DNA; 18 BP.
XX
AC   AAS14018;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PTEN antisense oligonucleotide ISIS 29558.
XX
KW   Human; PTEN; MMAC1; TEP1; protein phosphatase; antisense; ss;
KW   antiinflammatory; cytostatic; antidiabetic; antilipaemic; infection;
KW   inflammation; tumour; diabetes; insulin resistance; insulin sensitivity;
KW   triglyceride control; cholesterol control; ISIS 29558.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /note= "Phosphorothioate backbone"
FT   modified_base    1. .4
FT                    /*tag=  b
FT                    /note= "Optionally 2'-methoxyethyl residue (2'-MOE). When
FT                    1-4 are 2'-MOE all cytosines in this region are 5-
FT                    methylcytosines"
FT   modified_base    15. .18
FT                    /*tag=  c
FT                    /note= "Optionally 2'-methoxyethyl residue (2'-MOE). When
FT                    15-18 are 2'-MOE all cytosines in this region are 5-
FT                    methylcytosines"
XX
PN   US6284538-B1.
XX
PD   04-SEP-2001.
XX
PF   24-MAY-2000; 2000US-00577902.
XX
PR   21-JUL-1999;   99US-00358381.
PR   14-DEC-1999;   99WO-US029594.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM,  Mckay R;
XX
DR   WPI; 2001-588976/66.
XX
PT   New antisense oligonucleotides targeting nucleic acids encoding PTEN,
PT   useful for treating diabetes, increasing insulin sensitivity, or
PT   decreasing insulin resistance, blood triglyceride or cholesterol levels
PT   in a diabetic animal.
XX
PS   Example 15; Col 41; 38pp; English.
XX
CC   The invention relates to a compound targeted to a nucleic acid encoding
CC   PTEN (a dual specificity protein phosphatase), where the compound is an
CC   antisense oligonucleotide. The antisense oligonucleotides are useful in
CC   modulating the function of nucleic acids encoding PTEN, ultimately
CC   modulating the amount of PTEN produced. The antisense compounds can used
CC   as diagnostics, therapeutics, prophylactics (e.g. to prevent or delay
CC   infection, inflammation or tumour formation), and as research agents and
CC   kits. The antisense compounds are also useful in treating diabetes,
CC   decreasing insulin resistance, increasing insulin sensitivity and
CC   decreasing blood triglyceride or cholesterol levels in a diabetic animal.
CC   The present sequence is an antisense oligonucleotide targetting the DNA
CC   encoding PTEN (also known as MMAC1/TEP1)
XX
SQ   Sequence 18 BP; 6 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        406 TCTACGTGATCGAGA 420
              ||||  ||||||  |||
Db         18 TCTATGTGATCAAGA 4


RESULT 1162
AAH39010
ID   AAH39010 standard; DNA; 18 BP.
XX
```

AC AAH39010;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 1806.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 59; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 66 CTGCACTACGAGGGC 80
|| ||| ||||||||
Db 3 CTTCACCACGAGGGC 17

RESULT 1163
AAF61776/c
ID AAF61776 standard; DNA; 18 BP.
XX
AC AAF61776;
XX
DT 26-JUL-2001 (first entry)
XX
DE M. bacterium katG PCR primer MYC-33.
XX
KW PCR primer; katG; isoniazide resistance; mycobacteria; detection; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN DE19943911-A1.
XX
PD 10-MAY-2001.
XX
PF 14-SEP-1999; 99DE-01043911.
XX
PR 16-NOV-1998; 98DE-01052696.
XX
PA (RIND/) RINDER H.
PA (ZAHL/) ZAHLER M.
PA (LOES/) LOESCHER T.
XX
PI Rinder H, Zahler M, Loescher T;
XX
DR WPI; 2001-301247/32.
XX
PT Predicting resistance to isoniazide in mycobacteria, useful for selection
PT of treatment, by detecting specific mutation in the katG resistance gene.
XX
PS Claim 1; Page 7; 10pp; German.
XX
CC This invention describes a novel method, which does not require a culture
CC stage, for predicting resistance to isoniazide in mycobacteria, isolated
CC from clinical material, based on detecting a mutation in codon 315 of the
CC katG resistance gene. A part of this gene is amplified by nested
CC polymerase chain reaction (PCR) and the mutation is detected using a
CC restriction endonuclease (RE). The method is used to predict isoniazide
CC resistance in clinical isolates of mycobacteria, to assist selection of
CC appropriate therapy. The method is simple and quick; does not require a
CC lengthy preliminary culture step; detects over 99% of resistance-causing
CC mutations in codon 315, and the only apparatus needed is a PCR
CC instrument, thermostat and gel electrophoresis system, making it suitable
CC for routine use in non-specialized laboratories. When the preferred RE,
CC AciI, is used, the amplicon includes two other AciI sites that serve as
CC internal controls, allowing false positives (caused by a faulty
CC restriction reaction) to be avoided. This sequence represents the PCR
CC primer MYC-33 which is used in the detection method described in the
CC invention
XX
SQ Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 36 GACGAAGATGGCCAC 50
||||| | |||||||
Db 17 GACGATGCTGGCCAC 3

RESULT 1164
AAC99259/c
ID AAC99259 standard; DNA; 18 BP.
XX
AC AAC99259;
XX
DT 06-MAR-2001 (first entry)
XX
DE Probe sequence used in probe array SEQ ID 19.
XX
KW Probe; probe array; probe-combined substrate; detection; ss.
XX

```
OS   Synthetic.
XX
PN   JP2000270896-A.
XX
PD   03-OCT-2000.
XX
PF   28-JAN-1999;   99JP-00019915.
XX
PR   28-JAN-1999;   99JP-00019915.
XX
PA   (CANO ) CANON KK.
XX
DR   WPI; 2001-027424/04.
XX
PT   A preparation of a probe-combined substrate, a probe array, detection of
PT   a target substance, specification of the base sequence of a single-
PT   stranded nucleic acid in a sample, and determination of a target
PT   substance in a sample.
XX
PS   Example 3; Page 15; 20pp; Japanese.
XX
CC   This invention relates to a probe-combined substrate, a probe array, and
CC   a method for the detection of a target substance in a sample. The probe
CC   array can be used for detecting a target substance with high reliability.
CC   Sequences AAC99241 - AAC99305 represent probes used in an array in an
CC   example illustrating the invention
XX
SQ   Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        297 AAGGACCTGAGCCCC 311
              | | ||||||||||||
Db         18 ATGAACCTGAGCCCC 4


RESULT 1165
AAS10228
ID   AAS10228 standard; DNA; 18 BP.
XX
AC   AAS10228;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Antisense oligonucleotide for human integrin alpha 4, ISIS 24449.
XX
KW   Integrin alpha 4; antisense; very late antigen 4; VLA4;
KW   autoimmune disease; inflammatory disease; rheumatoid arthritis;
KW   multiple sclerosis; tumour metastasis; melanoma; asthma; psoriasis;
KW   allergy; Grave's disease; Hashimoto's thyroiditis; oligonucleotide;
KW   systemic lupus erythematosus; allograft rejection; ISIS 24449; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Other= all cytosines are 5-methyl cytosine"
FT   modified_base   1. .18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Other= Phosphorothioate backbone"
FT   modified_base   1. .4
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Other= 2' methoxyethoxy residues"
FT   modified_base   5. .14
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "Other= 2' deoxy residues"
FT   modified_base   15. .18
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "Other= 2' methoxyethoxy residues"
XX
PN   US6258790-B1.
XX
PD   10-JUL-2001.
XX
PF   19-AUG-1999;   99US-00377309.
XX
PR   05-OCT-1998;   98US-00166203.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Condon TP,  Cowsert LM;
XX
DR   WPI; 2001-450381/48.
XX
PT   Composition for treating inflammatory and autoimmune diseases, comprises
PT   antisense compound targeted to nucleic acid molecule encoding integrin
PT   alpha4 and inhibit expression of integrin alpha4.
XX
PS   Example 8; Col 25; 49pp; English.
XX
CC   The sequence is an antisense oligonucleotide targetting human integrin 4,
CC   a protein involved in autoimmune and inflammatory diseases. The invention
CC   relates to antisense inhibitors of integrin alpha 4 which target and
CC   inhibit expression of integrin alpha 4. The antisense molecules are
CC   useful for inhibiting the expression of integrin alpha4 in human cells or
CC   tissues, treating an animal having a disease or condition associated with
CC   expression of integrin alpha4, e.g., inflammatory disease or condition,
CC   autoimmune disease or condition including rheumatoid arthritis, multiple
CC   sclerosis and tumour metastases, melanoma, asthma, psoriasis, allergy,
CC   Grave's disease, Hashimoto's thyroiditis, systemic lupus erythematosus
CC   and allograft rejection, and diseases or conditions characterised by
CC   leukocyte migration into affected tissues, preferably central nervous
CC   system tissues. The antisense molecules are also useful for reducing the
CC   levels of VLA-4 and alpha4beta7 integrin in human cells or tissues, and
CC   reducing the adherence of cells of a first type e.g., melanoma cells or
CC   lymphocytes, to cells of a second type e.g., endothelial cells, by
CC   inhibiting integrin alpha4 expression and thus decreasing adhesion of
CC   cells
XX
SQ   Sequence 18 BP; 2 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         98 CACGTCTGACCGCGA 112
              ||||||| ||| ||
Db          2 CACGTCTGGCCGGGA 16


RESULT 1166
AAD19348/c
ID   AAD19348 standard; DNA; 18 BP.
XX
AC   AAD19348;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Mammalian PAC93.1 DNA sequencing reverse PCR primer, Int6R.
XX
KW   Interleukin-12; IL-12 p40; autoimmune disease; Th1/Th2 dysregulation;
KW   therapy; allelic variant; insulin dependant diabetes mellitus; IDDM;
KW   PCR primer; ss.
XX
OS   Mammalia.
XX
PN   WO200173035-A1.
```

```
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-AU000340.
XX
PR   27-MAR-2000; 2000AU-00006466.
PR   15-MAY-2000; 2000US-0204366P.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Morahan G;
XX
DR   WPI; 2001-611629/70.
XX
PT   Screening mammals for autoimmune diseases such as diabetes, comprises
PT   identifying polymorphisms in interleukin (IL)-12 p40.
XX
PS   Disclosure; Page 44; 115pp; English.
XX
CC   The patent discloses a method of screening mammals for autoimmune
CC   diseases by identifying polymorphisms in interleukin (IL)-12 p40 gene.
CC   The methods and kits of the invention are used for screening individuals,
CC   families and populations for disease conditions or predispositions for
CC   the development of a disease condition which is characterised,
CC   exacerbated or associated with Th1/Th2 dysregulation in a mammal. They
CC   are used to treat, prevent or diagnose autoimmune diseases such as IDDM
CC   (Insulin dependant diabetes mellitus). The present DNA sequence is
CC   reverse PCR primer, Int6R used for sequencing mammalian PAC93.1 DNA which
CC   is used as a template for determining the complete IL-12 p40 genomic
CC   sequence
XX
SQ   Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        260 CACGGTGCACCTGGA 274
              | | ||||||||||||
Db         15 CTCAGTGCACCTGGA 1


RESULT 1167
AAD19276/c
ID   AAD19276 standard; DNA; 18 BP.
XX
AC   AAD19276;
XX
DT   18-DEC-2001  (first entry)
XX
DE   PCR primer #2, to detect polymorphism in mammalian IL-12 p40 exon 7.
XX
KW   Interleukin-12; IL-12 p40; autoimmune disease; Th1/Th2 dysregulation;
KW   therapy; Taq1+ allelic variant; insulin dependant diabetes mellitus;
KW   IDDM; PCR primer; ss.
XX
OS   Mammalia.
XX
PN   WO200173035-A1.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-AU000340.
XX
PR   27-MAR-2000; 2000AU-00006466.
PR   15-MAY-2000; 2000US-0204366P.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Morahan G;
XX
DR   WPI; 2001-611629/70.
XX
PT   Screening mammals for autoimmune diseases such as diabetes, comprises
PT   identifying polymorphisms in interleukin (IL)-12 p40.
XX
PS   Example 6; Page 41; 115pp; English.
XX
CC   The patent discloses a method of screening mammals for autoimmune
CC   diseases by identifying polymorphisms in interleukin (IL)-12 p40 gene.
CC   The methods and kits of the invention are used for screening individuals,
CC   families and populations for disease conditions or predispositions for
CC   the development of a disease condition which is characterised,
CC   exacerbated or associated with Th1/Th2 dysregulation in a mammal. They
CC   are used to treat, prevent or diagnose autoimmune diseases such as IDDM
CC   (Insulin dependant diabetes mellitus). The present DNA sequence is a PCR
CC   primer which is used for detecting polymorphism in mammalian IL-12 p40
CC   exon 7
XX
SQ   Sequence 18 BP; 4 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        260 CACGGTGCACCTGGA 274
              | | ||||||||||||
Db         15 CTCAGTGCACCTGGA 1


RESULT 1168
ABK72456/c
ID   ABK72456 standard; DNA; 18 BP.
XX
AC   ABK72456;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Sample origonucleotide #18 for analysing nucleic acid base sequence.
XX
KW   Nucleic acid base sequence analysis; DNA diagnosis; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200233068-A1.
XX
PD   25-APR-2002.
XX
PF   18-OCT-2000; 2000WO-JP007244.
XX
PR   18-OCT-2000; 2000WO-JP007244.
XX
PA   (CANO ) CANON KK.
XX
PI   Yamamoto N,  Okamoto T,  Suzuki T;
XX
DR   WPI; 2002-372310/40.
XX
PT   Screening an unknown base sequence at a defined site of a target single-
PT   stranded nucleic acid for use in DNA diagnosis and therapy, comprises a
PT   DNA chip, fluorescence yield and pattern-based method.
XX
PS   Example 1; Page 13; 53pp; Japanese.
XX
CC   The present invention relates to a method of analysing an unknown nucleic
CC   acid base sequence. The method comprises preparing a probe array,
CC   hybridising with the probe array, measuring the fluorescence yield in the
CC   reaction, obtaining a template pattern, producing a sample pattern, and
CC   comparing the sample pattern with the template pattern. The method is
CC   useful for specifying an unknown base sequence at a defined site of a
CC   target single-stranded nucleic acid, which is useful for analysing a
CC   nucleic acid base sequence. The method is applicable in DNA diagnosis and
CC   therapy, and is useful in medicine and biology. Measuring the
CC   fluorescence yield allows the detection of a one-base mismatch which can
CC   be considered to produce high detection accuracy. The hybrid pattern of
CC   the DNA probe is used so the difference in thermostability is less
```

```
CC   important, and the judgement on each spot can be reliably carried out.
CC   ABK72439-ABK72502 represent sample origonucleotides used in the present
CC   invention
XX
SQ   Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        297 AAGGACCTGAGCCCC 311
              | | ||||||||||||
Db         18 ATGAACCTGAGCCCC 4


RESULT 1169
ABN99764/c
ID   ABN99764 standard; DNA; 18 BP.
XX
AC   ABN99764;
XX
DT   20-AUG-2002  (first entry)
XX
DE   DNA probe #18 for use in an oligonucleotide array.
XX
KW   Human; probe; array; oligonucleotide detection; ss.
XX
OS   Synthetic.
XX
PN   JP2002065274-A.
XX
PD   05-MAR-2002.
XX
PF   31-AUG-2000; 2000JP-00263395.
XX
PR   31-AUG-2000; 2000JP-00263395.
XX
PA   (CANO ) CANON KK.
XX
DR   WPI; 2002-474199/51.
XX
PT   Detection of an object component in a sample using an oligonucleotide as
PT   detecting probe.
XX
PS   Example 3; Page 19; 25pp; Japanese.
XX
CC   The invention relates to a novel method for detecting a complex formed
CC   between a probe and its complement. The method is used for detecting a
CC   complex formed between an oligonucleotide of known base sequence and a
CC   complementary probe, and for evaluating if the sequence is contained in
CC   liquid samples, or the level of binding by using the oligonucleotide as
CC   the detecting probe. The sequence represents a probe used in the
CC   invention
XX
SQ   Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        297 AAGGACCTGAGCCCC 311
              | | ||||||||||||
Db         18 ATGAACCTGAGCCCC 4


RESULT 1170
ABK86809/c
ID   ABK86809 standard; DNA; 18 BP.
XX
AC   ABK86809;
XX
DT   24-SEP-2002  (first entry)
XX
DE   FMO gene expression vector sequencing primer (EcoRI).
XX
KW   YUCCA; FMA; flavin-containing monooxygenase; ss; primer; sequncing;
KW   plant; hypocotyl elongation; root thickness; root hair development;
KW   lateral root initiation; apical dominance; epinastic leaf growth;
KW   flowering node formation; fruit yield; auxin levels;
KW   root development alteration.
XX
OS   Unidentified.
XX
PN   WO200240689-A2.
XX
PD   23-MAY-2002.
XX
PF   13-NOV-2001; 2001WO-US043462.
XX
PR   16-NOV-2000; 2000US-00715834.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Zhao Y,  Chory J,  Fankhauser C,  Weigel D,  Cashman J;
XX
DR   WPI; 2002-508330/54.
XX
PT   Enhancing a plant trait for studying biochemical pathways, comprises
PT   transforming a plant with an expression vector having a sequence encoding
PT   flavin-containing monooxygenase, expressing the monooxygenase and
PT   measuring the trait.
XX
PS   Example 2; Page 21; 41pp; English.
XX
CC   This invention relates to a method for enhancing a trait in a plant. The
CC   method comprises transforming a plant with an expression vector
CC   comprising a nucleotide sequence encoding a flavin-containing
CC   monooxygenase (FMO), expressing FMO, and measuring the trait. The method
CC   of the invention is useful for enhancing a trait (such as increased
CC   hypocotyl elongation, root thickness, root hair development, lateral root
CC   initiation, apical dominance, epinastic leaf growth, flowering node
CC   formation, fruit yield, auxin levels (preferably endogenous auxin
CC   levels), and growth and yield, parthenocarpic fruit production or root
CC   development alteration, where the increased root development is selected
CC   from increased root length, root diameter, rate of elongation, root hair
CC   development, and anthocyanin content) in a plant, preferably a
CC   monocotyledonous or a dicotyledonous plant, more preferably A. thaliana
CC   or a tobacco plant. The method of the invention is useful for studying
CC   biochemical pathways such as the interaction between two growth
CC   regulators or root development, and for oxidising xenobiotics in plants.
CC   The present sequence represents a sequencing primer used to sequence the
CC   flaven-containing monooxygenase (FMO) YUCCA expression vector of the
CC   invention
XX
SQ   Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match              2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        118 GCAAGTACGGCATGC 132
              ||||| |||| ||||
Db         18 GCAAGAACGGAATGC 4


RESULT 1171
AAD40969
ID   AAD40969 standard; DNA; 18 BP.
XX
AC   AAD40969;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Human PI3K p85 antisense oligonucleotide ISIS #28017.
XX
KW   Human; antisense; PI3K p85; obesity; type 2 diabetes; cancer; tumour;
```

```
KW   prophylaxis; hyperproliferative condition; infection; inflammation;
KW   therapy; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1. .4
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   3
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   15. .18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   15. .16
FT                   /*tag=  e
FT                   /mod_base= m5c
XX
PN   WO200240637-A2.
XX
PD   23-MAY-2002.
XX
PF   19-NOV-2001; 2001WO-US045006.
XX
PR   20-NOV-2000; 2000US-00715983.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM,  Murray SF,  Butler MM,  Dean NM;
XX
DR   WPI; 2002-519374/55.
XX
PT   Antisense compounds targeted against polynucleotides encoding PI3K p85
PT   useful for treating e.g. cancer, Type 2 diabetes, obesity.
XX
PS   Claim 3; Page 79; 121pp; English.
XX
CC   The invention relates to antisense compounds targetted to a nucleic acid
CC   molecule encoding PI3K p85 to inhibits its expression. Antisense
CC   compounds of the invention are used for treating obesity, Type 2 diabetes
CC   and hyperproliferative condition e.g. cancer. They may also be useful
CC   prophylactically, e.g. to prevent or delay infection, inflammation or
CC   tumour formation. Antisense compounds either alone or in combination with
CC   other antisense compounds or therapeutics can be used as tools in
CC   differential and/or combinatorial analyses to elucidate expression
CC   patterns of a portion or the entire complement of genes expressed within
CC   cells and tissues. They are commonly used as research reagents and
CC   diagnostics. The present sequence is an antisense oligonucleotide
CC   targetted to human PI3K p85 DNA
XX
SQ   Sequence 18 BP; 1 A; 6 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        362 CTTCCTCACTTTCCT 376
              |||| || |||||||
Db          3 CTTCTTCTCTTTCCT 17


RESULT 1172
ABL54918/c
ID   ABL54918 standard; DNA; 18 BP.
XX
AC   ABL54918;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human tumour suppressor gene p53 probe #18.
XX
KW   Human; p53; probe; variation detection; DNA array; ss.
XX
OS   Homo sapiens.
XX
PN   EP1184467-A2.
XX
PD   06-MAR-2002.
XX
PF   31-AUG-2001; 2001EP-00307415.
XX
PR   31-AUG-2000; 2000JP-00263396.
XX
PA   (CANO ) CANON KK.
XX
PI   Yamamoto N,  Okamoto T,  Tanaka S,  Suzuki T;
XX
DR   WPI; 2002-271043/32.
XX
PT   Screening for gene variation by using DNA array in which probes giving
PT   strong signals forming hybrids with normal sequence, and probes having
PT   sequences expected to form hybrids with variants are separately arranged.
XX
PS   Example 2; Page 6; 22pp; English.
XX
CC   The sequence represents a two-base mismatch probe designed to detect a
CC   variation a specific base in the p53 gene sequence. The invention relates
CC   to a novel method for screening for a variation in a nucleic acid
CC   sequence. The method involves using a DNA array in which a group of
CC   probes which will give strong signals forming hybrids with a normal gene
CC   sequence, and a group of probes having sequences expected to form hybrids
CC   with gene variants are separately arranged. The method is useful for
CC   screening for the presence or absence of variation in a nucleic acid
CC   sequence. The method is also useful for mass screening to determine
CC   rapidly the presence or absence of a gene variation without need of an
CC   expensive apparatus and a complex analysis
XX
SQ   Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        297 AAGGACCTGAGCCCC 311
              | | ||||||||||||
Db         18 ATGAACCTGAGCCCC 4


RESULT 1173
ABS78179/c
ID   ABS78179 standard; DNA; 18 BP.
XX
AC   ABS78179;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #663.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
```

XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 31; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 18 BP; 0 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 379 ACCGCGACGACGGCG 393
||||| |||||||
Db 15 ACCGCCGCGACGGCG 1

RESULT 1174
AAS17140/c
ID AAS17140 standard; DNA; 18 BP.
XX
AC AAS17140;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human acid sensing ion channel subunit 3, ASIC3A, RT-PCR primer #1.
XX
KW Human; ss; acid sensing ion channel; ASIC3A; analgesic; anti-HIV;
KW neuroprotective; nootropic; antiparkinsonian; anticonvulsant;
KW cerebroprotective; cardiant; antianginal; hypotensive; RT-PCR primer;
KW antiatherosclerotic; vasotropic; tranquiliser; antidepressant;
KW chronic pain; neuropathic pain; diabetes; cancer; AIDS;
KW acquired immunodeficiency syndrome; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW Creutzfeldt-Jacob disease; amyotrophic lateral sclerosis; dementia;
KW convulsion; epilepsy; stroke; anxiety; depression; angina;
KW cardiovascular disease; congestive heart failure; vasoconstriction;
KW hypertension; atherosclerosis; restenosis; bleeding; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200181570-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-CA000561.
XX
PR 20-APR-2000; 2000CA-02304494.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Seguela P, Babinski K;
XX
DR WPI; 2002-055353/07.
XX
PT New heteromultimeric proton-gated ion channel for diagnosing, treating
PT diseases associated with expression of the channel e.g. neurodegenerative
PT diseases, comprises two different types of acid sensing ion channel
PT subunits.
XX
PS Example 3; Page 102; 105pp; English.
XX
CC The invention relates to a protein complex forming a heteromultimeric
CC amiloride-and gadolinium-sensitive proton-gated cation channel (ASIC-
CC 2S.2), where the individual components of the heteromultimeric channel
CC include the acid sensing ion channel (ASIC)2A and ASIC3 protein or their
CC variants having 80% sequence identity, the channel being activated by
CC protons, acids, low pH solutions, the nucleic acids encoding the
CC subunits, a recombinant bicistronic vector comprising a nucleic acid
CC encoding at least two individual subunits or variants of ASIC-2S.2, a
CC host cell comprising the vector, an antibody raised against one of the
CC subunits or a domain which is capable of disrupting assembly of the ion
CC channel and ant/agonists of the ion channel. The polypeptides and
CC polynucleotides are useful for diagnosing a disease or a susceptibility
CC to a disease in a subject related to expression or activity of the
CC heteromultimeric channel (e.g. by gene therapy using the vector). Such
CC diseases include chronic pain, neuropathic pain such as diabetic-, cancer
CC - and AIDS (acquired immunodeficiency syndrome)-related,
CC neurodegenerative diseases such as Alzheimer's disease, Parkinson's
CC disease, Huntington's disease, Creutzfeldt-Jacob disease, and amyotrophic
CC lateral sclerosis and dementias, including AIDS-related as well as
CC convulsions, epilepsy, stroke, anxiety and depression. They are also
CC useful for treating cardiovascular diseases such as angina, congestive
CC heart failure, vasoconstriction, hypertension, atherosclerosis,
CC restenosis and bleeding. ASIC-2S.2 plays a role in the regulation of
CC neurotransmitter release, neuronal excitability or excitotoxicity and is
CC useful in screening for compounds that regulate neurotransmitter release,
CC synaptic efficacy, neuroexcitability or neurotoxicity. The present
CC sequence is an RT (reverse transcriptase) PCR primer used to measure the
CC tissue distribution of mRNA encoding human ASIC3A
XX
SQ Sequence 18 BP; 3 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 36 GACGAAGATGGCCAC 50
|| |||| |||||||
Db 16 GAGGAAGGTGGCCAC 2

RESULT 1175
ABL38809/c
ID ABL38809 standard; DNA; 18 BP.
XX
AC ABL38809;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 190.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX

PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 144; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 18 BP; 0 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 379 ACCGCGACGACGGCG 393
||||| |||||||
Db 15 ACCGCCGCGACGGCG 1

RESULT 1176
ABS60920/c
ID ABS60920 standard; DNA; 18 BP.
XX
AC ABS60920;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human genotyping PCR primer #73.
XX
KW Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;
KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedaema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW viral infection; bacterial infection; fungal infection; COPD;
KW Chronic obstructive pulmonary disease; enterocolitis.
XX
OS Homo sapiens.
XX
PN WO200261131-A2.
XX
PD 08-AUG-2002.
XX
PF 03-DEC-2001; 2001WO-US047235.
XX
PR 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
XX
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
XX
DR WPI; 2002-619265/66.
XX
PT New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
PS Example 3; Page 900; 977pp; English.
XX
CC The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridises to a
CC polymorphic position as provided in the detailed summary of single
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC obtaining the sample from one or more individuals and determining the
CC nucleic acid sequence at one or more polymorphic positions in a gene
CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC ; (4) identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the
CC nucleotide present in at least one polymorphic position, and comparing at
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC and compositions are useful for detecting, diagnosing, treating,
CC preventing various disorders such as angioedaema and diseases which
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC disease, trachomas, and cardiovascular diseases like angina pectoris,
CC hypertension, heart failure, myocardial infarction, ventricular
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC artery disease, arteriosclerosis and/or atherosclerosis, and
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence is a genotyping PCR primer
CC for the gene encoding one of the proteins listed above
XX
SQ Sequence 18 BP; 1 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 297 AAGGACCTGAGCCCC 311
|||| ||||| ||||
Db 16 AAGGCCCTGAACCCC 2

```
RESULT 1177
ABS60947
ID   ABS60947 standard; DNA; 18 BP.
XX
AC   ABS60947;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human genotyping PCR primer #100.
XX
KW   Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;
KW   BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
KW   kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW   angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KW   polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW   cardiovascular disease; angina pectoris; hypertension; heart failure;
KW   myocardial infarction; ventricular hypertrophy; vascular disease;
KW   aneurysm; embolism; thrombosis; coronary artery disease; angioedaema;
KW   arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW   autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW   viral infection; bacterial infection; fungal infection; COPD;
KW   Chronic obstructive pulmonary disease; enterocolitis.
XX
OS   Homo sapiens.
XX
PN   WO200261131-A2.
XX
PD   08-AUG-2002.
XX
PF   03-DEC-2001; 2001WO-US047235.
XX
PR   04-DEC-2000; 2000US-0251015P.
PR   23-JAN-2001; 2001US-0263678P.
PR   02-MAR-2001; 2001US-0273037P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA   (TSUC/) TSUCHIHASHI Z.
PA   (HUIL/) HUI L.
XX
PI   Tsuchihashi Z,  Hui L,  Zerba KE,  Ma-Edmonds M,  Perrone MH;
PI   Swanson BN,  Powell JR;
XX
DR   WPI; 2002-619265/66.
XX
PT   New isolated nucleic acid with at least one polymorphic position, useful
PT   for detecting, diagnosing and treating disorders such as angioedema,
PT   cancer, viral, bacterial or fungal infection, cardiovascular and
PT   autoimmune diseases.
XX
PS   Example 3; Page 905; 977pp; English.
XX
CC   The invention relates to an isolated nucleic acid from a human gene
CC   encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
CC   tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC   1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC   2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC   polymorphic position. Also included are (1) a probe that hybridises to a
CC   polymorphic position as provided in the detailed summary of single
CC   nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC   sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC   obtaining the sample from one or more individuals and determining the
CC   nucleic acid sequence at one or more polymorphic positions in a gene
CC   encoding a protein selected from the group above; (3) constructing (M2)
CC   haplotypes using the genes comprising grouping at least two nucleic acids
CC   ; (4) identifying (M3) an individual at risk of developing a disorder
CC   upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC   using the polymorphic data; (5) a library of nucleic acids, each of which
CC   comprises one or more polymorphic positions within a gene encoding a
CC   human protein selected from the group above; and (6) genotyping (M4) an
CC   individual comprising obtaining a nucleic acid sample, determining the
CC   nucleotide present in at least one polymorphic position, and comparing at
CC   least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC   and compositions are useful for detecting, diagnosing, treating,
CC   preventing various disorders such as angioedaema and diseases which
CC   involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC   disease, trachomas, and cardiovascular diseases like angina pectoris,
CC   hypertension, heart failure, myocardial infarction, ventricular
CC   hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC   artery disease, arteriosclerosis and/or atherosclerosis, and
CC   hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC   arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC   obstructive pulmonary disease (COPD) and enterocolitis (many other
CC   diseases and disorders are listed in the specification). The
CC   polynucleotides are also useful for chromosome identification. Antibodies
CC   against the proteins may be utilised for immunophenotyping of cell lines
CC   and biological samples. The present sequence is a genotyping PCR primer
CC   for the gene encoding one of the proteins listed above
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        266 GCACCTGGAGCAGGG 280
              ||||||||||  |||
Db          3 GCACCTGGAGTTGGG 17


RESULT 1178
ABS60977/c
ID   ABS60977 standard; DNA; 18 BP.
XX
AC   ABS60977;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human genotyping PCR primer #130.
XX
KW   Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;
KW   BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
KW   kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW   angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
KW   polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW   cardiovascular disease; angina pectoris; hypertension; heart failure;
KW   myocardial infarction; ventricular hypertrophy; vascular disease;
KW   aneurysm; embolism; thrombosis; coronary artery disease; angioedaema;
KW   arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
KW   autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
KW   viral infection; bacterial infection; fungal infection; COPD;
KW   Chronic obstructive pulmonary disease; enterocolitis.
XX
OS   Homo sapiens.
XX
PN   WO200261131-A2.
XX
PD   08-AUG-2002.
XX
PF   03-DEC-2001; 2001WO-US047235.
XX
PR   04-DEC-2000; 2000US-0251015P.
PR   23-JAN-2001; 2001US-0263678P.
PR   02-MAR-2001; 2001US-0273037P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA   (TSUC/) TSUCHIHASHI Z.
PA   (HUIL/) HUI L.
XX
PI   Tsuchihashi Z,  Hui L,  Zerba KE,  Ma-Edmonds M,  Perrone MH;
PI   Swanson BN,  Powell JR;
XX
DR   WPI; 2002-619265/66.
XX
PT   New isolated nucleic acid with at least one polymorphic position, useful
PT   for detecting, diagnosing and treating disorders such as angioedema,
PT   cancer, viral, bacterial or fungal infection, cardiovascular and
```

```
PT   autoimmune diseases.
XX
PS   Example 3; Page 909; 977pp; English.
XX
CC   The invention relates to an isolated nucleic acid from a human gene
CC   encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
CC   tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC   1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC   2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
CC   polymorphic position. Also included are (1) a probe that hybridises to a
CC   polymorphic position as provided in the detailed summary of single
CC   nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC   sequence; (2) analysing (M1) at least one nucleic acid sample comprising
CC   obtaining the sample from one or more individuals and determining the
CC   nucleic acid sequence at one or more polymorphic positions in a gene
CC   encoding a protein selected from the group above; (3) constructing (M2)
CC   haplotypes using the genes comprising grouping at least two nucleic acids
CC   ; (4) identifying (M3) an individual at risk of developing a disorder
CC   upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
CC   using the polymorphic data; (5) a library of nucleic acids, each of which
CC   comprises one or more polymorphic positions within a gene encoding a
CC   human protein selected from the group above; and (6) genotyping (M4) an
CC   individual comprising obtaining a nucleic acid sample, determining the
CC   nucleotide present in at least one polymorphic position, and comparing at
CC   least one position with a known data set. The genes, (M1, M2, M3 and M4)
CC   and compositions are useful for detecting, diagnosing, treating,
CC   preventing various disorders such as angioedaema and diseases which
CC   involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
CC   disease, trachomas, and cardiovascular diseases like angina pectoris,
CC   hypertension, heart failure, myocardial infarction, ventricular
CC   hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
CC   artery disease, arteriosclerosis and/or atherosclerosis, and
CC   hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
CC   arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC   obstructive pulmonary disease (COPD) and enterocolitis (many other
CC   diseases and disorders are listed in the specification). The
CC   polynucleotides are also useful for chromosome identification. Antibodies
CC   against the proteins may be utilised for immunophenotyping of cell lines
CC   and biological samples. The present sequence is a genotyping PCR primer
CC   for the gene encoding one of the proteins listed above
XX
SQ   Sequence 18 BP; 0 A; 10 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         29 GGGCTGGGACGAAGA 43
              |||| |||||| |||
Db         17 GGGCAGGGACGGAGA 3


RESULT 1179
AAD40053/c
ID   AAD40053 standard; DNA; 18 BP.
XX
AC   AAD40053;
XX
DT   22-OCT-2002  (first entry)
XX
DE   Human PTEN antisense oligonucleotide, ISIS 29598.
XX
KW   Human; phosphoinositide phosphatase; PTEN; liver; kidney; cholesterol;
KW   metabolic disease; diabetes; hyperproliferative; glucose; insulin; PEPCK;
KW   triglyceride; antisense gene therapy; cytostatic; adipose cell;
KW   antiproliferative; antisense; phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .18
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   modified_base    1. .4
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    15. .18
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   US2002058638-A1.
XX
PD   16-MAY-2002.
XX
PF   11-JUN-2001; 2001US-00878582.
XX
PR   21-JUL-1999;   99US-00358381.
PR   14-DEC-1999;   99WO-US029594.
PR   24-MAY-2000; 2000US-00577902.
XX
PA   (MONI/) MONIA B P.
PA   (COWS/) COWSERT L M.
PA   (MCKA/) MCKAY R.
XX
PI   Monia BP,  Cowsert LM,  Mckay R;
XX
DR   WPI; 2002-479187/51.
XX
PT   New compound, preferably an antisense oligonucleotide, that hybridizes
PT   and inhibits the expression of phosphoinositide phosphatase (PTEN), for
PT   treating diseases such as diabetes, or a hyperproliferative condition.
XX
PS   Example 15; Page 34; 39pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of phosphoinositide phosphatase (PTEN). The
CC   antisense compound is used to inhibit the expression of PTEN in cells or
CC   tissues, preferably human, or rodent, such as mouse or rat, liver, kidney
CC   or adipose cells or tissues. It is used to treat a disease or condition
CC   associated with PTEN, such as a metabolic disease or condition,
CC   preferably diabetes, especially Type 2 diabetes, or a hyperproliferative
CC   condition. It is also used to decrease blood glucose or insulin levels in
CC   an animal, preferably a diabetic human or rodent. It is also used to
CC   inhibit expression of PEPCK in cells or tissues. It is also used to
CC   decrease insulin resistance, or increase insulin sensitivity, in an
CC   animal, preferably a diabetic human or rodent. It is used to decrease
CC   blood triglyceride or cholesterol levels in an animal, preferably a
CC   diabetic human or rodent. It is also used in antisense gene therapy. The
CC   present sequence is an antisense oligonucleotide targetted to human PTEN
CC   DNA
XX
SQ   Sequence 18 BP; 6 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        406 TCTACGTGATCGAGA 420
              |||| |||||| |||
Db         18 TCTATGTGATCAAGA 4


RESULT 1180
ABL43688/c
ID   ABL43688 standard; DNA; 18 BP.
XX
AC   ABL43688;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 1p36-35 PCR primer SEQ ID NO:732.
XX
```

```
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-00068285.
XX
PR   10-MAR-2000; 2000JP-00066716.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (GENO-) GENOTEX YG.
XX
DR   WPI; 2002-144136/19.
XX
PT   Arraying genome clones.
XX
PS   Claim 4; Page 19; 528pp; Japanese.
XX
CC   The present invention describes a method of arraying genome clones. The
CC   method comprises: (a) clones of the genomic libraries contained in
CC   multiwell plates numbered for discrimination are mixed in each of the
CC   multiwell plates; (b) a primer designed based on the chromosome marker
CC   sequence is added to the mixture to carry out an amplification reaction;
CC   (c) a signal corresponding to the marker is detected from the resultant
CC   amplified product to specify the discrimination Nos. of the multiwell
CC   plates containing the clones having said marker sequence; (d) the order
CC   of the markers is changed so that the same discrimination Nos. succeed to
CC   the maximum in the specified discrimination Nos. to array the multiwell
CC   plates; (e) the clones in the multiwell plates of the specified
CC   discrimination Nos. are mixed respectively in each wells of longitudinal
CC   and lateral directions; (f) the mixed clones are cultured and the
CC   resultant cultures are amplified by using the above primer; (g) signals
CC   are detected from the amplified products; (h) the clones in the multiwell
CC   plates are specified from the detected result; and (i) the clones are
CC   reconstituted as the positions on the chromosome and arrayed. The
CC   microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC   PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC   represent PCR primers for human chromosome 21q22.1, which are
CC   specifically claimed for use in the present invention
XX
SQ   Sequence 18 BP; 5 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        270 CTGGAGCAGGGCGGC 284
              ||||||||| | |||
Db         18 CTGGAGCAGTGTGGC 4


RESULT 1181
ABL44670
ID   ABL44670 standard; DNA; 18 BP.
XX
AC   ABL44670;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 1p36-35 PCR primer SEQ ID NO:1714.
XX
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-00068285.
XX
PR   10-MAR-2000; 2000JP-00066716.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (GENO-) GENOTEX YG.
XX
DR   WPI; 2002-144136/19.
XX
PT   Arraying genome clones.
XX
PS   Claim 4; Page 38; 528pp; Japanese.
XX
CC   The present invention describes a method of arraying genome clones. The
CC   method comprises: (a) clones of the genomic libraries contained in
CC   multiwell plates numbered for discrimination are mixed in each of the
CC   multiwell plates; (b) a primer designed based on the chromosome marker
CC   sequence is added to the mixture to carry out an amplification reaction;
CC   (c) a signal corresponding to the marker is detected from the resultant
CC   amplified product to specify the discrimination Nos. of the multiwell
CC   plates containing the clones having said marker sequence; (d) the order
CC   of the markers is changed so that the same discrimination Nos. succeed to
CC   the maximum in the specified discrimination Nos. to array the multiwell
CC   plates; (e) the clones in the multiwell plates of the specified
CC   discrimination Nos. are mixed respectively in each wells of longitudinal
CC   and lateral directions; (f) the mixed clones are cultured and the
CC   resultant cultures are amplified by using the above primer; (g) signals
CC   are detected from the amplified products; (h) the clones in the multiwell
CC   plates are specified from the detected result; and (i) the clones are
CC   reconstituted as the positions on the chromosome and arrayed. The
CC   microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC   PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC   represent PCR primers for human chromosome 21q22.1, which are
CC   specifically claimed for use in the present invention
XX
SQ   Sequence 18 BP; 6 A; 7 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         83 CGCAGTGGACATCAC 97
              | ||| |||||||||
Db          1 CACAGCGGACATCAC 15


RESULT 1182
ABS54297
ID   ABS54297 standard; DNA; 18 BP.
XX
AC   ABS54297;
XX
DT   05-DEC-2002  (first entry)
XX
DE   Pig SOX9 cDNA, PCR primer #2.
XX
KW   Pig; tissue repair; progenitor cell; bioresorbable bead; chondrocyte;
KW   gel forming substance; embryonic stem cell; bone marrow stromal cell;
KW   tissue damage; articular cartilage degeneration; primary osteoarthritis;
KW   articular cartilage damage; sporting injury; tissue augmentation; trauma;
KW   cosmetic; scar; facial wrinkle; tissue growth; osteopathic;
KW   antiarthritic; dermatological; PCR; primer; ss; SOX9.
XX
OS   Sus sp.
XX
PN   WO200262357-A1.
XX
PD   15-AUG-2002.
XX
PF   04-FEB-2002; 2002WO-AU000106.
XX
PR   05-FEB-2001; 2001AU-00002896.
```

XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (INTE-) IND TECHNOLOGY RES INST.
XX
PI Werkmeister JA, Tsai W, Ramshaw JAM, Thissen HW, Chang K;
XX
DR WPI; 2002-723146/78.
XX
PT New device having tissue-like characteristics, useful for treating
PT diseased or damaged tissue, e.g. articular cartilage degeneration
PT associated with primary osteoarthritis, or for tissue augmentation for
PT cosmetic purposes.
XX
PS Example 20; Page 18; 52pp; English.
XX
CC The present invention relates to methods and devices for tissue repair.
CC The devices have tissue-like characteristics for treating diseased or
CC damaged tissue or for augmenting tissue in a subject. The device
CC comprises cells of type(s) normally found in healthy tissue corresponding
CC to the diseased or damaged tissue or in the tissue to be augmented,
CC and/or its suitable progenitor cells in association with bioresorbable
CC beads or particles, and optionally a gel and/or gel forming substance.
CC The cells and/or suitable progenitor cells are chondrocytes, embryonic
CC stem cells, and/or bone marrow stromal cells. The devices and methods are
CC useful for treating diseased or damaged tissue in a subject, such as
CC articular cartilage degeneration associated with primary osteoarthritis,
CC or other articular cartilage damage caused by sporting injuries or
CC trauma. They are also useful for tissue augmentation for cosmetic
CC purposes, e.g. treatment of scars or facial wrinkles. The present devices
CC and methods provide treatment that is less traumatic than previous art.
CC The use of biodegradable polymers in the device offer advantages over non
CC -degradable polymers in that their gradual degradation steadily creates
CC room for tissue growth and eliminate the need for surgical removal of the
CC scaffolds following restoration of the articular cartilage. Another
CC advantage is its ability to be administered by injection if desired. The
CC beads or particles provide mechanical and space-filling benefits while
CC tissue regeneration is progressing, by offering physical support and
CC resistance to compression. The present sequence represents a PCR primer
CC used to amplify pig SOX9 cDNA, in the examples of the present invention
XX
SQ Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 88 TGGACATCACCACGT 102
||||||| |||||
Db 3 TGGACATCCACACGT 17

RESULT 1183
ABT04711/c
ID ABT04711 standard; DNA; 18 BP.
XX
AC ABT04711;
XX
DT 27-SEP-2002 (first entry)
XX
DE End-labelled probe array production method-related oligonucleotide 18.
XX
KW End-labelled probe array production; probe; ss; target substance capture.
XX
OS Unidentified.
XX
PN JP2002153284-A.
XX
PD 28-MAY-2002.
XX
PF 24-NOV-2000; 2000JP-00357446.
XX
PR 24-NOV-2000; 2000JP-00357446.
XX
PA (CANO) CANON KK.
XX
DR WPI; 2002-552742/59.
XX
PT Preparation of an end-labelled probe array, for capturing a target
PT substance.
XX
PS Example 1; Page 5; 25pp; Japanese.
XX
CC The invention comprises a method for the synthesis of an end-labelled
CC probe array - in which part of a probe for capturing a target substance
CC is fixed at a plural of the matrix sites on the surface of a probe array
CC substrate. In the method of the invention the units for constituting the
CC probe are combined successively and, at the final stage of the successive
CC synthesis, a labelling substance is combined to the end of the probe and
CC extended to a desired chain length. The method of the invention is useful
CC for the production of a probe array. The present DNA sequence represents
CC an oligonucleotide that was used in an example of the invention
XX
SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 297 AAGGACCTGAGCCCC 311
| | ||||||||||||
Db 18 ATGAACCTGAGCCCC 4

RESULT 1184
ABL31388/c
ID ABL31388 standard; DNA; 18 BP.
XX
AC ABL31388;
XX
DT 21-MAR-2002 (first entry)
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 877.
XX
KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX
OS Homo sapiens.
XX
PN WO200192572-A1.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-JP004662.
XX
PR 01-JUN-2000; 2000JP-00164798.
XX
PA (NISN) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
XX
PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX
DR WPI; 2002-122074/16.
XX
PT Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
XX
PS Claim 10; Page 259; 345pp; Japanese.
XX
CC The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of

```
CC   individuals by determining immunogenetic differences before transplanting
CC   between them, providing genetic information to decide compatibility of
CC   organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC   pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC   diagnosis of genetic diseases and identifying individuals
XX
SQ   Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        394 CCAAGAAGGTCTTCT 408
              ||||||  | ||||||
Db         16 CCAAGAGGTTCTTCT 2


RESULT 1185
ABL59653/c
ID   ABL59653 standard; DNA; 18 BP.
XX
AC   ABL59653;
XX
DT   18-JUL-2002  (first entry)
XX
DE   Oligonucleotide probe SEQ ID NO:18.
XX
KW   Simultaneous determination; probe; ss.
XX
OS   Synthetic.
XX
PN   JP2002065299-A.
XX
PD   05-MAR-2002.
XX
PF   31-AUG-2000; 2000JP-00263505.
XX
PR   31-AUG-2000; 2000JP-00263505.
XX
PA   (CANO ) CANON KK.
XX
DR   WPI; 2002-398978/43.
XX
PT   Simultaneous testing of the reactivity of a sample with other different
PT   samples, comprises applying to the two samples to a substrate comprising
PT   divided matrices.
XX
PS   Example 1; Page 11; 24pp; Japanese.
XX
CC   The present invention describes a method for determining simultaneously
CC   the reactivity of a first sample with other samples, in which the second
CC   to the 2 plus nth (n is not less than 1) samples having different
CC   properties are arranged independently on a substrate, on whose surface
CC   the first sample is already present, and the reactivities between the
CC   first sample and each of the second to the 2 plus n-th samples are
CC   determined. Also described is a tissue sample matrix in which several
CC   samples from different sources are present on each matrix divided on a
CC   substrate. The method is used for determining simultaneously the
CC   reactivity of a first sample with several other differing samples.
CC   ABL59636 to ABL59701 represent oligonucleotide probes used in an example
CC   from the present invention
XX
SQ   Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        297 AAGGACCTGAGCCCC 311
              | | ||||||||||||
Db         18 ATGAACCTGAGCCCC 4


RESULT 1186
ABT06232/c
ID   ABT06232 standard; DNA; 18 BP.
XX
AC   ABT06232;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Synthetic DNA selling system - related oligonucleotide 37.
XX
KW   synthetic DNA selling system; internet; ss; purchase order menu;
KW   major histocompatibility complex; MHC.
XX
OS   Synthetic.
XX
PN   JP2002074089-A.
XX
PD   12-MAR-2002.
XX
PF   29-AUG-2000; 2000JP-00259715.
XX
PR   29-AUG-2000; 2000JP-00259715.
XX
PA   (CANO ) CANON KK.
XX
DR   WPI; 2002-492955/53.
XX
PT   Synthetic DNA selling system using the Internet, displays purchase order
PT   menu to orderer's terminal and initiates production of selected DNA for
PT   the successful bidder.
XX
PS   Disclosure; Fig 5; 22pp; Japanese.
XX
CC   The invention comprises a synthetic DNA selling system using the
CC   internet. The system displays a purchase order menu display, with the
CC   number of base sequences of DNA from which the orderer selects a DNA. The
CC   order information is transmitted to a successful bidder side server which
CC   orders for production and delivery of selected synthetic DNA. The system
CC   of the invention is useful for marketing synthetic DNAs of different base
CC   sequences and concentrations according to the desire of the user,
CC   especially genes concerned with human major histocompatibility complex
CC   (MHC). Oligonucleotides ABT06196 - ABT06278 are used in the invention
XX
SQ   Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        297 AAGGACCTGAGCCCC 311
              | | ||||||||||||
Db         18 ATGAACCTGAGCCCC 4


RESULT 1187
ABZ98176/c
ID   ABZ98176 standard; DNA; 18 BP.
XX
AC   ABZ98176;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human CD23 + A1261 oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
```

PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13418; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 18 BP; 1 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 45 GGCCACCACTCAGAG 59
|| |||||| |||||
Db 17 GGACACCACACAGAG 3

RESULT 1188
ABX34365/c
ID ABX34365 standard; DNA; 18 BP.
XX
AC ABX34365;
XX
DT 11-FEB-2003 (first entry)
XX
DE PCR primer #2 for S. atroolivaceus leinamycin gene cluster ORF lnmC.
XX
KW Leinamycin biosynthesis gene cluster; Lmn; open reading frame; ORF;
KW anti-tumour antibiotic; broad spectrum antimicrobial activity;
KW Gram-positive; Gram-negative bacteria; chemical modification; metabolite;
KW apo-carrier protein; holo-carrier protein; tumour; polyketide;
KW hybrid polypeptide/polyketide metabolite; Lnm production; cytostatic;
KW PCR; primer; ss.
XX
OS Streptomyces atroolivaceus.
XX

PN WO200277179-A2.
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-US008937.
XX
PR 26-MAR-2001; 2001US-0278935P.
XX
PA (REGC) UNIV CALIFORNIA.
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shen B, Cheng Y, Tang G;
XX
DR WPI; 2003-018907/01.
XX
PT Novel gene cluster responsible for synthesis of leinamycin in
PT Streptomyces atroolivaceus useful for making various peptide and/or
PT polyketide, and/or hybrid polypeptide/polyketide metabolites.
XX
PS Claim 1; Page 28; 185pp; English.
XX
CC The present invention relates to the isolation of the Streptomyces
CC atroolivaceus leinamycin (Lnm) biosynthesis gene cluster containing 71
CC open reading frames (ORFs) (ORFs -35 through -1, ORFs lnmA through lnmZ,
CC and ORFs +1 through +9). Leinamycin is a novel anti-tumour antibiotic
CC produced by several Streptomyces species. It exhibits broad spectrum
CC antimicrobial activity against Gram-positive and Gram-negative bacteria,
CC but not against fungi. The polypeptides encoded by the Lnm biosynthesis
CC gene cluster ORFs are useful for chemically modifying a molecule in a
CC host cell. The host cell is a bacterium or eukaryotic cell, including a
CC mammalian, yeast, plant, fungal, or insect cell. The molecule is an
CC endogenous metabolite produced by the host cell or exogenously supplied
CC metabolite, or an amino acid, and the polypeptide is a peptide synthetase
CC or amino transferase. The polypeptides encoded by the Lmn gene cluster
CC are useful for converting an apo-carrier protein to a holo-carrier
CC protein. Lnm shows potent antitumour activity in tumour models in vivo.
CC The Lnm gene cluster modules and/or catalytic domains are useful for
CC making various peptide and/or polyketide, and/or hybrid
CC polypeptide/polyketide metabolites. The proteins encoded by the ORFs are
CC useful alone, or in combination with other active domains to modify
CC various target substrates. The Lmn gene cluster is useful to upregulate
CC endogenous Lnm production to permit Lnm production in cells and/or to
CC make various modified Lnm. Lnm, its analogue, or other polyketide,
CC peptide or hybrid polyketide/peptide metabolites are useful as
CC therapeutic agents, to treat a number of disorders, depending upon the
CC type of metabolites. ABX34290-ABX34431 represent PCR primers used to
CC amplify individual ORFs of the S. atroolivaceus leinamycin biosynthesis
CC gene cluster
XX
SQ Sequence 18 BP; 4 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTGCGGGTGACCGAG 29
||| ||||| |||||
Db 18 CTGTGGGTGGCCGAG 4

RESULT 1189
ABZ84114
ID ABZ84114 standard; DNA; 18 BP.
XX
AC ABZ84114;
XX
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant rat PCR primer #1273.
XX
KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS Rattus sp.

```
OS   Synthetic.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 332; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
CC   predicting and determining toxicological responses on a cellular, organ
CC   or system level. The arrays comprising the human genes are useful for
CC   toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ   Sequence 18 BP; 2 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         20 GGTGACCGAGGGCTG 34
              | |||| ||||||||
Db          3 GCTGACTGAGGGCTG 17


RESULT 1190
ABZ84057
ID   ABZ84057 standard; DNA; 18 BP.
XX
AC   ABZ84057;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Toxicologically relevant rat PCR primer #1216.
XX
KW   Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX
OS   Rattus sp.
OS   Synthetic.
XX
PN   WO2003016500-A2.
XX
PD   27-FEB-2003.
XX
PF   16-AUG-2002; 2002WO-US026514.
XX
PR   16-AUG-2001; 2001US-0313080P.
XX
PA   (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI   Neft RE,  Dunn RT,  Adkins K,  Pickett GG,  Kier LD,  Schmeiser K;
PI   Alen P;
XX
DR   WPI; 2003-268322/26.
XX
PT   Determining a toxicological response to an agent, useful for screening of
PT   drugs, comprises comparing the expression profile of one or more human
PT   toxic response genes to a reference gene expression profile indicative of
PT   toxicity.
XX
PS   Claim 1; Page 329; 455pp; English.
XX
CC   The present invention describes a method (M1) for determining a
CC   toxicological response to an agent, which comprises comparing the
CC   expression profile of one or more human toxic response genes to a
CC   reference gene expression profile indicative of toxicity, and so
CC   determining the presence of a toxic response to the agent. Also
CC   described: (1) an array comprising one or more polynucleotides selected
CC   from the genes corresponding to the partial sequences given in ABZ82842
CC   to ABZ84764, or their fragments of at least 20 nucleotides; or homologues
CC   ; and (2) determining if a gene putatively identified to be a toxic
CC   response gene plays a role on toxic response pathways by determining the
CC   expression profile of the gene after exposure of cells or a human subject
CC   to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC   exposing cells to an agent or isolating cells from a human subject who
CC   was exposed to an agent; (b) obtaining the test gene expression profile
CC   for a putatively identified toxic response gene after exposure to a known
CC   toxic pharmaceutical or industrial agent; and (c) comparing the test
CC   profile to the expression profile of a gene with a similar function or
CC   comparing the test profile to the expression profile of that gene after
CC   exposure to other known toxic compounds. The methods are useful for
CC   predicting and determining toxicological responses on a cellular, organ
CC   or system level. The arrays comprising the human genes are useful for
CC   toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ   Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        267 CACCTGGAGCAGGGC 281
              || |||||||| |||
Db          4 CATCTGGAGCATGGC 18


RESULT 1191
ABS56993
ID   ABS56993 standard; DNA; 18 BP.
XX
AC   ABS56993;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Implantation serine proteinase 1 (ISP1) RT-PCR primer #2.
XX
KW   Implantation serine proteinase 1; ISP1; female infertility; gene therapy;
KW   contraception; reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200281665-A2.
XX
```

PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-CA000474.
XX
PR 06-APR-2001; 2001US-0281724P.
PR 30-MAY-2001; 2001US-0294736P.
PR 25-JAN-2002; 2002US-0350962P.
XX
PA (RANC/) RANCOURT D E.
PA (RANC/) RANCOURT S L.
PA (OSUL/) O'SULLIVAN C M.
XX
PI Rancourt DE, Rancourt SL, O'sullivan CM;
XX
DR WPI; 2003-058536/05.
XX
PT New purified Implantation Serine Proteinase protein for diagnosing,
PT treating or ameliorating female infertility by modulating the process of
PT hatching and implantation of the embryo.
XX
PS Example; Page 40; 85pp; English.
XX
CC The invention describes a purified Implantation Serine Proteinase (ISP)
CC protein. The ISP protein is useful in diagnosing, treating or
CC ameliorating female infertility (e.g. using gene therapy), particularly
CC by modulating the process of hatching and implantation of the embryo. The
CC ISP protein inhibitor is useful as contraception. This sequence
CC represents a reverse transcriptase PCR primer used to isolate DNA
CC encoding implantation serine proteinase 1 (ISP1) from embryo and
CC placental tissue
XX
SQ Sequence 18 BP; 6 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 36 GACGAAGATGGCCAC 50
| | ||||||||||
Db 1 GTCAAAGATGGCCAC 15

RESULT 1192
AAD52135
ID AAD52135 standard; DNA; 18 BP.
XX
AC AAD52135;
XX
DT 02-MAY-2003 (first entry)
XX
DE Xanthomonas citri AEH DNA specific primer #3.
XX
KW Alpha-amino ester hydrolase; AEH; beta-lactam antibiotic; enzyme;
KW EC 3.1.1.43; primer; ss.
XX
OS Xanthomonas citri.
XX
PN WO200286111-A2.
XX
PD 31-OCT-2002.
XX
PF 24-APR-2002; 2002WO-EP004536.
XX
PR 25-APR-2001; 2001US-0286766P.
XX
PA (STAM) DSM NV.
XX
PI Van Der Laan JM, Polderman-Tijmes JJ, Barends TRM;
XX
DR WPI; 2003-103410/09.
XX
PT Novel recombinantly produced alpha-amino ester hydrolase protein useful
PT in the production of beta-lactam antibiotics.
XX
PS Example 3; Page 43; 134pp; English.
XX
CC The present invention relates to alpha-amino ester hydrolase (AEH; alpha-
CC AEH; EC 3.1.1.43) proteins and polynucleotides encoding such proteins.
CC Sequences of the invention are useful in the production of beta-lactam
CC antibiotics. The present sequence is Xanthomonas citri AEH DNA specific
CC primer. This sequence is used in the exemplification of the invention
XX
SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 ACCGAGGGCTGGGAC 38
||||| | |||||||
Db 1 ACCGATGCCTGGGAC 15

RESULT 1193
ACD99950/c
ID ACD99950 standard; DNA; 18 BP.
XX
AC ACD99950;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #636.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 26; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 18 BP; 0 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 2.8%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        379 ACCGCGACGACGGCG 393
              ||||| ||||||||
Db         15 ACCGCCGCGACGGCG 1


RESULT 1194
AAD58047/c
ID   AAD58047 standard; DNA; 18 BP.
XX
AC   AAD58047;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Dehalococcoides family A group 16S rDNA amplifying primer, RpDhcAO1213.
XX
KW   16S rDNA; dechlorinating bacterial organism; PCR; primer; ss.
XX
OS   Dehalococcoides sp.
XX
PN   WO2003064695-A1.
XX
PD   07-AUG-2003.
XX
PF   30-JAN-2002; 2002WO-US003927.
XX
PR   30-JAN-2002; 2002WO-US003927.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Ebersole R,  Hendrickson E;
XX
DR   WPI; 2003-636804/60.
XX
PT   Novel isolated 16S rDNA sequence useful for forming probes and primers
PT   which are useful for identifying dechlorinating bacterial organism in
PT   various samples.
XX
PS   Claim 2; Page 52; 110pp; English.
XX
CC   The invention relates to an isolated 16S rDNA sequence indicative of a
CC   dechlorinating bacterial organism. The invention is useful for forming
CC   probes and primers which are useful for identifying dechlorinating
CC   bacterial organism in various samples. The method of the invention is
CC   useful for identifying a dechlorinating bacterial organism that is a
CC   member of a cell population or consortium. The isolated bacterial
CC   organism is useful for dechlorinating chlorinated compounds which
CC   involves contacting a chlorinated compound with the organism.
CC   Oligonucleotide polymer of the invention is useful for separating sub-
CC   families of dechlorinating bacterial organism. The present sequence is
CC   Dehalorespirating bacteria 16S rDNA amplifying PCR primer
XX
SQ   Sequence 18 BP; 1 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 CGGGTGACCGAGGGC 32
              |||||||||| | ||
Db         15 CGGGTGACCGGGAGC 1


RESULT 1195
ACF05368/c
ID   ACF05368 standard; DNA; 18 BP.
XX
AC   ACF05368;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Thermus igniterrae nucleic acid polymerase PCR primer.
XX
KW   Nucleic acid polymerase; enzyme; strand displacement amplification; PCR;
KW   primer extension; PCR; primer; ss.
XX
OS   Thermus spp.
XX
PN   WO2003048307-A2.
XX
PD   12-JUN-2003.
XX
PF   22-NOV-2002; 2002WO-US037650.
XX
PR   30-NOV-2001; 2001US-0334435P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Rozzelle J,  Bolchakova E;
XX
DR   WPI; 2003-513746/48.
XX
PT   New isolated Thermus igniterrae nucleic acid polymerases and nucleic
PT   acids encoding the polymerases, useful for DNA synthesis, primer
PT   extension, DNA sequencing, reverse transcription, or DNA and RNA
PT   amplification procedures.
XX
PS   Example 1; Page 47; 67pp; English.
XX
CC   The present sequence is that of a PCR primer based on a conserved region
CC   of Thermus aquaticus, Thermus thermophilus, Thermus filiformis, Thermus
CC   caldophilus and Thermus flavus nucleic acid polymerases. It was used as C
CC   -terminal primer, with the N-terminal primer given in ACF05367, in a PCR
CC   amplification of Thermus igniterrae strain ID RF-4 (ATCC 700962) DNA. A
CC   gene fragment was obtained, and subsequent PCRs yielded a full-length
CC   coding sequence (see ACF05363) for T. igniterrae nucleic acid polymerase.
CC   The invention provides nucleic acid polymerase polynucleotides, vectors,
CC   host cells and polypeptides, including mutants having reduced 5'-3'
CC   exonuclease activity and/or reduced bias against ddNTP incorporation. The
CC   wild-type and mutant enzymes are used in claimed methods for thermocyclic
CC   nucleic acid amplification, especially strand displacement amplification
CC   or PCR, and for primer extension
XX
SQ   Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        138 CGCCTGGCGGTGGAG 152
              | ||||| |||||||
Db         15 CCCCTGGAGGTGGAG 1


RESULT 1196
ADA50410/c
ID   ADA50410 standard; DNA; 18 BP.
XX
AC   ADA50410;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Thermus scotoductus nucleic acid polymerase PCR primer SEQ ID NO:35.
XX
KW   nucleic acid polymerase; enzyme; Thermus scotoductus; DNA polymerase;
KW   salt tolerance; thermostability; PCR primer; ss.
XX
OS   Synthetic.
OS   Thermus scotoductus.
XX
PN   WO2003066804-A2.
XX
PD   14-AUG-2003.
XX
PF   13-SEP-2002; 2002WO-US029102.
XX
PR   14-SEP-2001; 2001US-0322218P.
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PR   30-NOV-2001; 2001US-0334489P.
XX
PA   (APPL-) APPLERA CORP.
PA   (BOLC/) BOLCHAKOVA E V.
PA   (ROZZ/) ROZZELLE J E.
XX
PI   Bolchakova EV,  Rozzelle JE;
XX
DR   WPI; 2003-663590/62.
XX
PT   New nucleic acid encoding a Thermus scotoductus strain X-1, ATCC Deposit
PT   No. 27978 nucleic acid polymerase, useful for producing nucleic acid
PT   polymerases having e.g., improved sequence discrimination or better salt
PT   tolerance.
XX
PS   Example 1; Page 80; 179pp; English.
XX
CC   The present invention describes isolated nucleic acids encoding nucleic
CC   acid polymerases from Thermus scotoductus. ALso described: (1) an
CC   isolated nucleic acid (I) encoding a nucleic acid polymerase from Thermus
CC   scotoductus strain X-1, ATCC Deposit No. 27978; (2) an isolated DNA
CC   polymerase polypeptide from Thermus scotoductus strain X-1, ATCC Deposit
CC   No. 27978; (3) an isolated nucleic acid (II) comprising any of a set of
CC   12 nucleic acid sequences (S1, see ADA50425 to ADA50436) which encodes a
CC   nucleic acid polymerase; (4) an isolated nucleic acid (III) encoding a
CC   nucleic acid polymerase comprising any of a set of 16 amino acid
CC   sequences (S2, see ADA50389 to ADA50404); (5) isolated nucleic acid
CC   polymerases comprising any of amino acid sequences S2; (6) vectors
CC   comprising (I), (II), or (III), and especially expression vectors in
CC   which the nucleic acid polymerase gene is operably linked to a promoter;
CC   (7) a host cell comprising an isolated nucleic acid molecule encoding a
CC   nucleic acid polymerase from Thermus scotoductus strain X-1, ATCC Deposit
CC   No. 27978; (8) a host cell comprising (I) or (II); (9) a kit comprising a
CC   container containing a nucleic acid polymerase comprising any of amino
CC   acid sequences S2; (10) preparing (M1) a nucleic acid polymerase
CC   comprising any of amino acid sequences S2 by incubating a host cell
CC   comprising an encoding nucleic acid under conditions sufficient for RNA
CC   transcription and translation; (11) a nucleic acid polymerase prepared by
CC   M1; (12) synthesising DNA (M2) comprising contacting a polypeptide
CC   comprising any of amino acid sequences S2 with a DNA under conditions
CC   sufficient to permit DNA polymerisation; (13) a method (M3) for
CC   thermocyclic amplification of nucleic acid; and (14) a method (M4) of
CC   primer extension. The nucleic acid is useful for producing nucleic acid
CC   polymerases having improved sequence discrimination, better salt
CC   tolerance or varying degrees of thermostability with applications e.g. in
CC   PCR and DNA sequencing. The present sequence represents a PCR primer for
CC   Thermus scotoductus nucleic acid polymerase, which is used in an example
CC   from the present invention.
XX
SQ   Sequence 18 BP; 3 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        138 CGCCTGGCGGTGGAG 152
              | ||||| |||||||
Db         15 CCCCTGGAGGTGGAG 1


RESULT 1197
ADB36986/c
ID   ADB36986 standard; DNA; 18 BP.
XX
AC   ADB36986;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #600.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 14; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 18 BP; 0 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        379 ACCGCGACGACGGCG 393
              |||||  ||||||||
Db         15 ACCGCCGCGACGGCG 1


RESULT 1198
ADC99372/c
ID   ADC99372 standard; DNA; 18 BP.
XX
AC   ADC99372;
XX
DT   01-JAN-2004  (first entry)
XX
DE   PAMA forward PCR primer - SEQ ID 205.
XX
KW   cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;
KW   leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;
KW   VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;
KW   kinase insert domain protein receptor; EGFR; epidermal growth factor;
KW   FGFR1; fibroblast growth factor; Tie-1; PCR; ss; primer.
XX
OS   Unidentified.
XX
PN   WO2003035839-A2.
XX
PD   01-MAY-2003.
XX
PF   24-OCT-2002; 2002WO-US034021.
XX
PR   24-OCT-2001; 2001US-0345471P.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES INC.
XX
PI   Pillutla RC,  Brissette R,  Spruyt M,  Dedova O,  Blume A;
PI   Prendergast J,  Goldstein N;
XX
DR   WPI; 2003-457332/43.
```

```
XX
PT   Selecting target and target binder pairs for preparing a composition for
PT   treating cancer by mixing in a reaction vessel phage expressing
PT   biological targets and phage expressing target binders.
XX
PS   Example 18; SEQ ID NO 205; 172pp; English.
XX
CC   The invention relates to a novel method of selecting target and target
CC   binder pairs comprising mixing in a reaction vessel phage expressing
CC   biological targets and phage expressing target binders, each having
CC   distinguishable selection markers and selecting target and target binder
CC   pairs based on the selection markers. The molecules of the invention
CC   demonstrate cytostatic activity whilst the method may be useful for
CC   selecting target and target binder pairs for preparing a composition for
CC   treating cancer. Furthermore, the method may be utilised during gene
CC   therapy procedures. The current sequence is that of the PCR primer of the
CC   invention.
XX
SQ   Sequence 18 BP; 2 A; 9 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        336 GACCAGGGCCGGCTG 350
              | ||| |||||||||
Db         18 GGCCATGGCCGGCTG 4


RESULT 1199
ABH21732
ID   ABH21732 standard; DNA; 13 BP.
XX
AC   ABH21732;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 221709 for detecting SNP TSC0053962.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 221709; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 6 G; 1 T; 0 U; 1 Other;

  Query Match             2.7%;  Score 11.6;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 3.1e+02;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        231 AAATCGGGAGGC 242
              ||||||||||:
Db          2 AAATCGGGAGGY 13


RESULT 1200
ABH21733/c
ID   ABH21733 standard; DNA; 13 BP.
XX
AC   ABH21733;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 221710 for detecting SNP TSC0053962.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 221710; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 6 C; 1 G; 4 T; 0 U; 1 Other;

  Query Match             2.7%;  Score 11.6;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 3.1e+02;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        231 AAATCGGGAGGC 242
              ||||||||||:
```

```
Db          12 AAATCGGGAGGY 1


RESULT 1201
AAS98785
ID   AAS98785 standard; DNA; 15 BP.
XX
AC   AAS98785;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #151.
XX
KW   Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW   cytostatic; gene therapy; malignant histiocytosis; isogene;
KW   myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
KW   genotype; human; allele specific oligonucleotide; ASO; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179225-A2.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US012044.
XX
PR   12-APR-2000; 2000US-0196411P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-075058/10.
XX
PT   Novel polymorphic variants of colony stimulating factor 1 receptor useful
PT   in studying expression and function of the protein, useful for screening
PT   candidate drugs to treat diseases e.g. inflammatory disorders.
XX
PS   Claim 15; Page 17; 164pp; English.
XX
CC   The invention describes a novel isolated polynucleotide (I) comprising a
CC   sequence which is a polymorphic variant (PV) of a reference sequence for
CC   colony stimulating factor 1 receptor (CSF1R) gene, found on The
CC   polypeptide are useful for improving the discovery and development of
CC   drugs for treating diseases associated with CSF1R activity, e.g.,
CC   malignant histiocytosis, myeloid malignancies, and inflammatory disorders
CC   and the haplotypes can be used to validate CSF1R as a candidate target
CC   for treating a specific condition or disease predicted to be associated
CC   with CSF1R activity. Genotyping the CSF1R gene of an individual can also
CC   be used in developing diagnostic tests and therapeutic treatments. (I) is
CC   useful in studying the expression and function of CSF1R, and in
CC   expressing CSF1R protein for use in screening for candidate drugs to
CC   treat diseases related to CSF1R activity and in studying the effect of
CC   the variation on the biological activity of CSF1R as well as on the
CC   binding affinity of candidate drugs targeting CSF1R. Antibodies are
CC   useful in a variety of diagnostic and prognostic formats and therapeutic
CC   methods. A transgenic animal is useful in studying expression of the
CC   CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC   targeted against CSF1R protein, and for testing the efficacy of
CC   therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC   are useful as probes and primers, and for assaying a polymorphism in the
CC   target region. Without requiring any a priori knowledge of the phenotypic
CC   effect of any particular CSF1R or haplotype the invention provides a
CC   method for identifying lead compounds that are more likely to show
CC   efficacy in clinical trials. This sequence is an allele specific
CC   oligonucleotide primer used for detecting CSF1R gene polymorphisms,
CC   described in the method of the invention
XX
SQ   Sequence 15 BP; 2 A; 7 C; 4 G; 1 T; 0 U; 1 Other;

  Query Match             2.7%;  Score 11.6;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 4.2e+02;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        302 CCTGAGCCCCGG 313
              ||||||||||:|
Db          4 CCTGAGCCCCRG 15


RESULT 1202
AAS96144
ID   AAS96144 standard; DNA; 15 BP.
XX
AC   AAS96144;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human Acetylcholinesterase gene allele specific probe #7.
XX
KW   Human; ss; probe; allele specific oligonucleotide; ASO; ACHE;
KW   acetylcholinesterase; polymorphic variant; haplotyping; genotyping;
KW   neurological disease; Parkinson's disease; Alzheimer's disease; cancer;
KW   leukaemia; tumour; chromosome 7q22.
XX
OS   Homo sapiens.
XX
PN   WO200179219-A2.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011853.
XX
PR   14-APR-2000; 2000US-0197173P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (KAZE/) KAZEMI A.
XX
PI   Bentivegna SC,  Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-055248/07.
XX
PT   New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
PT   useful in expressing ACHE protein for use in screening for candidate
PT   drugs to treat diseases related to ACHE activity, e.g. neurological
PT   diseases or cancer.
XX
PS   Claim 16; Page 13; 79pp; English.
XX
CC   The invention relates to a polynucleotide comprising a polymorphic
CC   variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
CC   complement, the variant comprising an ACHE isogene defined by a haplotype
CC   selected from haplotypes 1-20 listed in the specification. Also included
CC   are methods for haplotyping and genotyping the ACHE gene of an
CC   individual, a method for predicting a haplotype pair for the ACHE gene of
CC   an individual, a method for identifying an association between a trait
CC   and at least one haplotype or haplotype pair of ACHE gene, recombinant
CC   nonhuman organisms transformed or transfected with the polynucleotide
CC   where the organism expresses ACHE protein encoded by the first nucleotide
CC   sequence or encoded by the polymorphic variant sequence, an isolated
CC   antibody specific for and immunoreactive with ACHE, a method of screening
CC   for drugs targeting the polypeptide contacting ACHE polymorphic variant
CC   with a candidate agent and assaying for binding activity, a computer
CC   system for storing and analysing polymorphism data for ACHE gene and a
CC   genome anthology for ACHE gene which comprises ACHE isogenes defined by
CC   haplotypes 1-20 given in the specification. The Polymorphisms are useful
CC   for studying the biological function of ACHE as well as in identifying
CC   drugs targeting this protein for the treatment of disorder related to its
CC   abnormal expression or function. The polymorphic variants may also be
CC   used in screening for compounds targeting ACHE to treat a specific
CC   condition or disease predicted to be associated with ACHE activity e.g.
CC   neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
CC   cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
CC   7q22. The present sequence is an allele specific oligonucleotide
CC   (ASO)probe used to detect the polymorphic ACHE variants of the invention
XX
SQ   Sequence 15 BP; 2 A; 6 C; 5 G; 1 T; 0 U; 1 Other;
```

```
  Query Match              2.7%;  Score 11.6;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 4.2e+02;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 AGGGCCGCGCAG 87
              |||||| |||||
Db          2 AGGGCCRCGCAG 13


RESULT 1203
ABA99313/c
ID   ABA99313 standard; DNA; 15 BP.
XX
AC   ABA99313;
XX
DT   13-MAY-2002  (first entry)
XX
DE   Human ALDH5 allele-specific oligonucleotide SEQ ID No 33.
XX
KW   ALDH5; human; gene; polymorphism; haplotype; aldehyde dehydrogenase 5;
KW   binding affinity; drug targeting; alcoholism; alcohol-induced disorder;
KW   antialcoholic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192279-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US017253.
XX
PR   26-MAY-2000; 2000US-0207508P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Finkel K,  Kazemi A,  Messer C,  Sanchis A;
XX
DR   WPI; 2002-122054/16.
XX
PT   New genetic variants with polymorphisms in the aldehyde dehydrogenase 5
PT   (ALDH5) gene, useful for studying the function of ALDH5, and for
PT   expressing ALDH5 protein which is useful in screening drugs for treating
PT   ALDH5-related diseases.
XX
PS   Claim 17; Page 80; 96pp; English.
XX
CC   This invention describes a novel isolated genes and haplotypes of the
CC   human aldehyde dehydrogenase 5 (ALDH5) gene containing polymorphic sites.
CC   The polymorphic ALDH5 variant is useful in studying the effect of the
CC   variation on the biological activity of ALDH5 and on the binding affinity
CC   of candidate drugs targeting ALDH5 for the treatment of alcoholism and
CC   alcohol-induced disorders. Polynucleotides comprising a polymorphic gene
CC   variant or fragment may be used for therapeutic purposes. ALDH5 protein
CC   isoforms may be used in assays to measure the binding affinities of one
CC   or more candidate drugs targeting the ALDH5 protein. ALDH5 proteins may
CC   be used to generate antibodies. Haplotyping method can be used by
CC   scientists to validate ALDH5 as a candidate target for treating a
CC   specific condition or disease predicted to be associated with ALDH5
CC   activity, and in the design of clinical trials of candidate drugs for
CC   treating a specific condition or disease predicted to be associated with
CC   ALDH5 activity. Information on polymorphisms on the ALDH5 gene can be
CC   applied for studying the biological function of ALDH5 as well as in
CC   identifying drugs targeting this protein for the treatment of disorders
CC   related to its abnormal expression or function. The products of the
CC   invention have antialcoholic activity. This sequence represents a human
CC   ALDH5 allele-specific oligonucleotide described in the disclosure of the
CC   invention
XX
SQ   Sequence 15 BP; 3 A; 5 C; 6 G; 0 T; 0 U; 1 Other;

  Query Match              2.7%;  Score 11.6;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 4.2e+02;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        244 GCTTCCCGGGCT 255
              :||||||||||||
Db         14 RCTTCCCGGGCT 3


RESULT 1204
ABA02229/c
ID   ABA02229 standard; DNA; 20 BP.
XX
AC   ABA02229;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Human/mouse C/EBP phosphorothioate antisense oligonucleotide, SEQ ID:41.
XX
KW   Human; C/EBP alpha; CCAAT/enhancer-binding protein alpha; CEBPA;
KW   transcription factor; tissue development; cellular function;
KW   proliferation; differentiation; adipocyte; energy metabolism;
KW   chondrogenic; ovulation; follicular development;
KW   hepatic steroid-induced cell cycle arrest; GLUT2 promoter regulation;
KW   hormonal metabolic regulation; granulocyte development; cancer;
KW   tumour formation; infection; inflammation; expression inhibition;
KW   antisense therapy; quantitative real-time PCR primer; ss.
XX
OS   Homo sapiens.
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
XX
PN   US6306655-B1.
XX
PD   23-OCT-2001.
XX
PF   13-JUN-2000; 2000US-00593589.
XX
PR   13-JUN-2000; 2000US-00593589.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Butler MM,  Wyatt J;
XX
DR   WPI; 2002-040202/05.
XX
PT   New antisense oligonucleotides for modulating the expression of
PT   CCAAT/Enhancer-binding proteins alpha, particularly useful for
PT   preventing, delaying or treating infection, inflammation or tumor
PT   formation.
XX
PS   Example 15; Col 42; 44pp; English.
XX
CC   Sequences ABA02205-ABA02282 represent antisense oligonucleotides targeted
CC   to the human CCAAT/enhancer-binding protein alpha (C/EBP alpha) gene,
CC   which inhibit its expression. The antisense oligonucleotides were
CC   designed to target different regions of the human C/EBP alpha RNA, and
CC   were analysed for their effect on C/EBP alpha mRNA levels by quantitative
CC   real-time PCR. A similar investigation on mouse C/EBP alpha expression
CC   was performed using a subset of the antisense oligonucleotides that were
```

CC capable of hybridising to mouse C/EBP alpha mRNA. The C/EBP family of
CC proteins are a family of transcription factors which regulate the
CC expression of wide range of genes that control normal tissue development,
CC cellular function, cellular proliferation and functional differentiation.
CC C/EBP alpha (also known as CEBPA) is primarily found in tissues involved
CC in energy metabolism which have a capacity to metabolise lipids,
CC cholesterol and other sterols. It is thought to be involved in the
CC regulation of adipocyte and chondrogenic differentation, and is also
CC involved in follicular development and ovulation, steroid-induced cell
CC cycle arrest in the liver, in controlling glucose transporter GLUT2
CC promoter activity, in the hormonal regulation of metabolism, and in
CC granulocyte development. The oligonucleotides of the invention are useful
CC for diagnosis, prevention and treatment of conditions associated with
CC C/EBP expression, such as cancer, tumour formation, infection, or
CC inflammation
XX
SQ Sequence 20 BP; 2 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.7%; Score 11.6; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 7.3e+02;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 266 GCACCTGGAGCAGGGCGG 283
||| |||| || || |||
Db 18 GCAGCTGGCGCTGGCCGG 1

RESULT 1205
AAF27039
ID AAF27039 standard; DNA; 38 BP.
XX
AC AAF27039;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:43.
XX
KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
KW bioavailibility; formulation; neurological disorder;
KW inflammatory disorder; autoimmune disorder; cancer;
KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
KW malignant glioma; medulloblastoma; neuroectodermal tumour;
KW mutagenic primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200073337-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014741.
XX
PR 01-JUN-1999; 99US-0137011P.
PR 13-AUG-1999; 99US-0149016P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Pepinsky RB, Taylor F, Garber E;
XX
DR WPI; 2001-049927/06.
XX
PT Modified hedgehog protein, useful in the treatment of Parkinson's disease
PT and Huntington's chorea, comprises a polymer containing a polyalkylene
PT glycol group linked to any residue other than the N-terminal and lysine
PT residues.
XX
PS Example 6; Page 77; 157pp; English.
XX
CC The invention relates to novel polymer conjugates of hedgehog proteins
CC which have increased bioavailability. The hedgehog proteins are
CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
CC glycol group, with the proviso that the polymer is not conjugated to the
CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
CC a hedgehog fusion protein. The invention also relates to methods of
CC defining and mapping functionally important regions of a protein by
CC modifying accessible amino acid side chains, and determining the effect
CC the position and/or type of modification have on the activity of the
CC protein. The hedgehog polymer conjugates may be used in the management of
CC various medical conditions including various neurological disorders,
CC inflammatory and autoimmune diseases, and cancers. In particular, they
CC may be used to prevent preventing or ameliorate neurodegenerative
CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
CC disease); age-associated neurological disease; neurological injury and
CC trauma; immunological diseases of the nervous system (e.g., multiple
CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
CC neuroectodermal tumours. The modifications made to the hedgehog protein
CC may result in increased half-life, altered tissue distribution (such as
CC an improved ability to stay in the vasculature for longer periods of
CC time), increased stability in solution, protection from proteolytic
CC degradation, or reduced immunogenicity. In particular, the ability to
CC remain in the vasculature for prolonged periods may allow a hedgehog
CC protein of the invention to cross the blood-brain barrier, and an
CC increased thermal stability would be an advantage when formulating the
CC hedgehog protein in powder form. The present sequence represents a human
CC Sonic hedgehog mutagenic primer used in an exemplification of the
CC invention
XX
SQ Sequence 38 BP; 8 A; 11 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 2.7%; Score 11.6; DB 1; Length 38;
Best Local Similarity 65.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 156 GGCTTCGACTGGGTGTACTACGAGTC 181
| ||| ||| | |||| | ||||
Db 13 GCCTTGCACTCGTAGTACACCCAGTC 38

Search completed: April 21, 2004, 12:31:04
Job time : 11 secs